

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 06-22-04
Searcher: Beverly C 2528
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CGW

This Page Blank (uspto)

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 09:36:12 ; Search time 14423 Seconds
(without alignments)
17495.885 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 cttgcacgacaggtttccg.....tgccgacattcaatgcag 5822

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:

2: gb_hgt:

3: gb_in:

4: gb_om:

5: gb_ov:

6: gb_pat:

7: gb_ph:

8: gb_pl:

9: gb_pr:

10: gb_ro:

11: gb_sts:

12: gb_sy:

13: gb_un:

14: gb_vi:

15: em_ba:

16: em_fun:

17: em_hum:

18: em_in:

19: em_mu:

20: em_om:

21: em_or:

22: em_ov:

23: em_pat:

24: em_ph:

25: em_pl:

26: em_ro:

27: em_sts:

28: em_un:

29: em_vi:

30: em_hgt_hum:

31: em_hgt_inv:

32: em_hgt_other:

33: em_hgt_mus:

34: em_hgt_pln:

35: em_hgt_rtd:

36: em_hgt_mam:

37: em_hgt_vrt:

38: em_sy:

39: em_hgt_hum:

40: em_hgt_mus:

41: em_hgt_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2892	49.7	4486	12	EVCOR116N	Z29589 Expression
2	2760.8	47.4	4412	12	EVCOR112N	Z29587 Expression
3	2755.6	47.3	5534	6	AR037157	AR037157 Sequence
4	2755.6	47.3	5534	6	AR112043	AR112043 Sequence
5	2705.8	46.5	4350	12	AF173954	AF173954 Cloning v
6	2705.8	46.5	5558	12	AF173955	AF173955 Cloning v
7	2686	46.1	4229	6	E63777	E63777 Method for
8	2683.4	46.1	3448	6	AX590988	AX590988 Sequence
9	2683.4	46.1	3448	6	AX591141	AX591141 Sequence
10	2683.4	46.1	3448	6	AX717564	AX717564 Sequence
11	2683.4	46.1	3551	12	AY122058	AY122058 Expressio
12	2677	46.0	3711	12	AF525778	AF525778 Expressio
13	2677	46.0	3033	12	CVGEM7LICF	U25272 Ligation-in
14	2677	46.0	3033	12	CVGEM7LICR	U25268 Ligation-in
15	2677	46.0	7823	12	AF041426	AF041426 Cloning v
16	2677	46.0	8658	12	AF338824	AF338824 Cloning v
17	2677	46.0	8696	12	AF379854	AF379854 Cloning v
18	2675.4	46.0	3018	6	A98767	A98767 Sequence 4
19	2671.6	45.9	3877	12	AB038599	AB038599 Cloning v
20	2671.6	45.9	6320	12	AB038600	AB038600 Cloning v
21	2668.6	45.8	4514	6	AX781452	AX781452 Sequence
22	2668.6	45.8	4514	6	AX816961	AX816961 Sequence
23	2658.4	45.7	9359	6	AX384394	AX384394 Sequence
24	2658.4	45.7	9359	6	AX473364	AX473364 Sequence
25	2654.6	45.6	2943	12	AF092940	AF092940 Cloning v
26	2654.6	45.6	3012	12	AF092546	AF092546 Cloning v
27	2641.4	45.4	2997	12	CVGEM7ZFP	X65310 Cloning vec
28	2641.4	45.4	3000	12	CVGEM5ZFP	X65308 Cloning vec
29	2641.4	45.4	3404	6	AX771236	AX771236 Sequence
30	2630.4	45.2	3485	6	AR199035	AR199035 Sequence
31	2553	43.9	6824	6	A25909	A25909 Synthetic Y
32	2552	43.8	10138	12	AF187951	AF187951 Activatio
33	2552	43.8	10450	12	AF218466	AF218466 Activatio
34	2551.8	43.8	37808	6	AX001082	AX001082 Sequence
35	2550	43.8	4883	6	AR220205	AR220205 Sequence
36	2550	43.8	4883	6	AX358365	AX358365 Sequence
37	2550	43.8	11038	12	AY196826	AY196826 Piggybac
38	2549	43.8	2958	6	AX247549	AX247549 Sequence
39	2549	43.8	2958	6	AX247550	AX247550 Sequence
40	2549	43.8	2958	6	AX247551	AX247551 Sequence
41	2549	43.8	2967	12	U02449	U02449 Cloning vec
42	2547.4	43.8	4133	12	U01668	U01668 Phagemid cl
43	2542.6	43.7	2959	12	AF118920	AF118920 Cloning v
44	2538.2	43.6	10597	6	AX006825	AX006825 Sequence
45	2538.2	43.6	10597	6	AX417673	AX417673 Sequence

ALIGNMENTS

RESULT 1
LOCUS EVCOR116N 4486 bp DNA linear SYN 24-MAR-1994
DEFINITION Expression vector pCOR116N (modified from pCOR116 in [3]).
ACCESSION Z29589.1 GI:452348
VERSION 229589
KEYWORDS ampicillin resistance; beta-lactamase; colE1 origin; expression vector; nos terminator; phage fl region; rice actin1 promoter.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 49 to 304)
AUTHORS Depicker, A., Stachel, S., Dhasee, P., Zambryski, P. and Goodman, H.M.
TITLE Napaline synthase: transcript and DNA sequence
JOURNAL J. Gen. Appl. Microbiol. 1, 561-573 (1982)

1343 TTCCATGATGAGCACTTTTAAAGTTCTGTATGTGCATACACTATTTATCCCGTATTGACG 1402
4217 CGGGCAAGAGCAACTCGGTGCGGCATACACTATTTCTCAGATGACTTGGTTGAGTACT 4276
1403 CGGGCAAGAGCAACTCGGTGCGGCAGGGGTTTCTCAGATGACTTGGTTGAGTACT 1462
4277 CACCACTCAGAAAAAGCATTTTACGATGGCATGACAGTAAGAGAAATTATGACAGTCTG 4336
1463 CACCACTCAGAAAAAGCATTTTACGATGGCATGACAGTAAGAGAAATTATGACAGTCTG 1522
4337 CATAACCATGATGATACACTCGGCCCACTTCTTGCAAAAGCATCGGAGGACCGA 4396
1523 CCATAACCATGATGATACACTCGGCCCACTTCTTGCAAAAGCATCGGAGGACCGA 1582
4397 AGGAGCTAACCGCTTTTTCACAAATGCGGGCATCATGTAACTCGGCTTTGATCGTTGGG 4456
1583 AGGAGCTAACCGCTTTTTCACAAATGCGGGCATCATGTAACTCGGCTTTGATCGTTGGG 1642
4457 AACCGGAGCTGAATGAAGCCATACCAAAAGAGCGGTGACACGATGCCCTGTAGCAA 4516
1643 AACCGGAGCTGAATGAAGCCATACCAAAAGAGCGGTGACACGATGCCCTGTAGCAA 1702
4517 TGGCAACAGCTTGGCGAACTTAACTCGCGAACTACTTACTAGCTTCCCGCAAC 4576
1703 TGGCAACAGCTTGGCGAACTTAACTCGCGAACTACTTACTAGCTTCCCGCAAC 1762
4577 AATTAAATAGACTGATGAGCGGATGAAAGTTGAGGACCACTTCTCGCTCGGCCCTTC 4636
1763 AATTAAATAGACTGATGAGCGGATGAAAGTTGAGGACCACTTCTCGCTCGGCCCTTC 1822
4637 CGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCA 4696
1823 CGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCA 1882
4697 TTGAGACCTGGCGGAGATGATGAGCGGTGAGCGGTGAGCGTGGGTCTCGCGGTATCA 4756
1883 TTGAGACCTGGCGGAGATGATGAGCGGTGAGCGGTGAGCGTGGGTCTCGCGGTATCA 1942
4757 GTGAGGCACTATGATGAGCAAGATGAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4816
1943 GTGAGGCACTATGATGAGCAAGATGAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2002
4817 AGCATTTGTAATCTGTGAGCAAGTGTGATCATATATATCTTATGATGATGATGATGATG 4876
2003 AGCATTTGTAATCTGTGAGCAAGTGTGATCATATATATCTTATGATGATGATGATGATG 2062
4877 ATTTTAAATTTAAAGGATCTAGGTGAGATCTTTTGTGATGATGATGATGATGATGATG 4936
2063 ATTTTAAATTTAAAGGATCTAGGTGAGATCTTTTGTGATGATGATGATGATGATGATG 2122
4937 CTTAAGCTGAGTTTTCGTTTCCACTGAGCGTCAAGCCCGGTAGAAAAGATCAAGATCTTT 4996
2123 CTTAAGCTGAGTTTTCGTTTCCACTGAGCGTCAAGCCCGGTAGAAAAGATCAAGATCTTT 2182
4997 CTTGAGATCTTTTTCGCGGTAATCTGCTGTGATGATGATGATGATGATGATGATGATG 5056
2183 CTTGAGATCTTTTTCGCGGTAATCTGCTGTGATGATGATGATGATGATGATGATGATG 2242
5057 CAGCGGTGTTTGTGTTGCGGATCAAGACTACCACTTTTTCGAGGTAATCTGCTGTGATG 5116
2243 CAGCGGTGTTTGTGTTGCGGATCAAGACTACCACTTTTTCGAGGTAATCTGCTGTGATG 2302
5117 TCAGGAGCGGAGATACCAATCTGCTTCTAGTGTAGCGGTAGTTAGGCGCACCACT 5176
2303 TCAGGAGCGGAGATACCAATCTGCTTCTAGTGTAGCGGTAGTTAGGCGCACCACT 2362
5177 TCAAGAACTCTGTAGCAGCGCTTACATACCTCGCTCTGCTTAATCTGTTTACAGTGGCTG 5236
2363 TCAGAACTCTGTAGCAGCGCTTACATACCTCGCTCTGCTTAATCTGTTTACAGTGGCTG 2422
5237 CTGCCAGTGGCGAATAGTGTGTTTACCGGGTGTGACTCAAGCATAGTATCCCGGATA 5296

2423 CTGCCAGTGGCGATAAGTGTGTCTTACCGGGTGTGACTCAAGACGATAGTTACCGGATA 2482
5297 AGCGCAGCGGTGCGGCTGAACGGGGGTTCGTGACACAGACCGCCAGCTTTGGAGCGAACGA 5356
2483 AGCGCAGCGGTGCGGCTGAACGGGGGTTCGTGACACAGACCGCCAGCTTTGGAGCGAACGA 2542
5357 CTTACACCCAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCGCCAGCTTTCCGGAAG 5416
2543 CTTACACCCAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCGCCAGCTTTCCGGAAG 2602
5417 GGAGAAAGCGGACAGGATTCGGTAAAGCGGAGGTGCGAAACAGGAGAGCGCACGAGGG 5476
2603 GGAGAAAGCGGACAGGATTCGGTAAAGCGGAGGTGCGAAACAGGAGAGCGCACGAGGG 2662
5477 AGCTTCCAGGGGAAACGCTGTATCTTTATAGTCTCTGTCGGGTTCGCGACCTCTGAC 5536
2663 AGCTTCCAGGGGAAACGCTGTATCTTTATAGTCTCTGTCGGGTTCGCGACCTCTGAC 2722
5537 TTGAGCGTGTGATTTTGTGATGCTCGTCAGGGGGGGAGCCCTATGGAAGAAAGCGCCAGCA 5596
2723 TTGAGCGTGTGATTTTGTGATGCTCGTCAGGGGGGGAGCCCTATGGAAGAAAGCGCCAGCA 2782
5597 ACGGCGCTTTTACAGGTTCTGCTGCGCTTTTGTGCGCTTTTGTCTCATCTTCTTCTG 5656
2783 ACGGCGCTTTTACAGGTTCTGCTGCGCTTTTGTGCGCTTTTGTCTCATCTTCTTCTG 2842
5657 CGTTATCCCTGATCTGTGATAACCGTATTTACCGCTTTTGTGAGTGTGAGTGTGAGTGTG 5716
2843 CGTTATCCCTGATCTGTGATAACCGTATTTACCGCTTTTGTGAGTGTGAGTGTGAGTGTG 2902
5717 GCGCAGACCGCAACGACGAGCGAGTCACTGAGCGAGGAGCGGAGGAGCGGAGCGCCCAA 5776
2903 GCGCAGACCGCAACGACGAGCGAGTCACTGAGCGAGGAGCGGAGGAGCGGAGCGCCCAA 2962
5777 TAGCAAAACCGCTCTCCCGCGGTGGCGGATTCATTATGCGAG 5822
2963 TAGCAAAACCGCTCTCCCGCGGTGGCGGATTCATTATGCGAG 3008

RESULT 2
EVCOR112N 4412 bp DNA linear SYN 18-MAR-1996
LOCUS Expression vector pCOR112N (modified from pCOR112 in [2]).
DEFINITION Z29587
ACCESSION Z29587.1 GI:452344
VERSION amplicillin resistance; beta-lactamase; coelI origin; expression
KEYWORDS vector; mos terminator; phage f1 region; rice actin1 promoter.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 27 to 282)
AUTHORS Depicker, A., Stachel, S., Dhaese, P., Zambryski, P. and Goodman, H.M.
TITLE Nopaline synthase: transcript mapping and DNA sequence
JOURNAL J. Mol. Appl. Genet. 1 (6), 561-573 (1982)
MEDLINE 83110651
PUBMED 7153689
REFERENCE 2
AUTHORS McElroy, D., Blowers, A.D., Jensen, B. and Wu, R.
TITLE Construction of expression vectors based on the rice actin 1 (Act1)
5' region for use in monocot transformation
JOURNAL Mol. Gen. Genet. 231 (1), 150-160 (1991)
MEDLINE 92092956
PUBMED 1753941
REMARK 3 (bases 1 to 4412)
REFERENCE 3 (bases 1 to 4412)
AUTHORS Liu, L., Dasgupta, I., Davies, J.W. and Hull, R.
TITLE Modified vectors for monocot transformation toward virus resistance
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 4412)
AUTHORS Liu, L.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1994) Liu L., John Innes Institute, Virus
Research, Colney Lane, Norwich, United Kingdom, NR4 7UH

4447 GATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCGATG 4506
1573 GATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCGATG 1632
4507 CCGTAGCAATGGCAACACGCTGGCAACACTATTAACCTGGCGAACTACTTACTCTAGCT 4566
1633 CCGTAGCAATGGCAACACGCTGGCAACACTATTAACCTGGCGAACTACTTACTCTAGCT 1692
4567 TCCCGCAACAATTAATAGACTGGATGGAGGGGGATAAAGTTGCAGGACCACTTCTGCGC 4626
1693 TCCCGCAACAATTAATAGACTGGATGGAGGGGGATAAAGTTGCAGGACCACTTCTGCGC 1752
4627 TCGGCCCTTCGGCTCGCTGGTTTATGCTGATPAATCTGGAGCCGGTGAGCTGGGTCT 4686
1753 TCGGCCCTTCGGCTCGCTGGTTTATGCTGATPAATCTGGAGCCGGTGAGCTGGGTCT 1812
4687 CGCGGTATCATTTGACAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTACTAC 4746
1813 CGCGGTATCATTTGACAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTACTAC 1872
4747 ACACGGGAGTCAGGCAACTATGGATGAACGAATAGACAGATCGCTGAGATAGTGCC 4806
1873 ACACGGGAGTCAGGCAACTATGGATGAACGAATAGACAGATCGCTGAGATAGTGCC 1932
4807 TCACTGATTAAGCAATTGGTAACTGTGACCAAGTTTACTCATATACTATTTAGATTGAT 4866
1933 TCACTGATTAAGCAATTGGTAACTGTGACCAAGTTTACTCATATACTATTTAGATTGAT 1992
4867 TTAACAATTCATTTTAAATTAAGGATCTAGTGAAGATCCCTTTTGGATATCTCATG 4926
1993 TTAACAATTCATTTTAAATTAAGGATCTAGTGAAGATCCCTTTTGGATATCTCATG 2052
4927 ACCAAATCCCTTAACTGAGTTTTCCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATC 4986
2053 ACCAAATCCCTTAACTGAGTTTTCCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATC 2112
4987 AAAGGATCTTTGAGATCCCTTTTTCCTGCGGTATCTGCTGCTTGCACCAACAAAAA 5046
2113 AAAGGATCTTTGAGATCCCTTTTTCCTGCGGTATCTGCTGCTTGCACCAACAAAAA 2172
5047 CCACCGCTACAGCGGTGGTTTGGTTCGGATCAAGAGCTACCACTCTTTTCCGAAG 5106
2173 CCACCGCTACAGCGGTGGTTTGGTTCGGATCAAGAGCTACCACTCTTTTCCGAAG 2232
5107 GTAACTGGCTTACGAGAGCGAGATACCAATATCTGCTTCTAGTGTAGCCGTAGTTA 5166
2233 GTAACTGGCTTACGAGAGCGAGATACCAATATCTGCTTCTAGTGTAGCCGTAGTTA 2292
5167 GGCCACCACTTCAAGAACTGTAGACCGGCTTACATCTGCTGCTGCTTAATCTGTTA 5226
2293 GGCCACCACTTCAAGAACTGTAGACCGGCTTACATCTGCTGCTGCTTAATCTGTTA 2352
5227 CCAGTGGCTGCTGCAGTGGCGATAAGTCTGCTTACCGGTTTGGATCTCAAGACGATG 5286
2353 CCAGTGGCTGCTGCAGTGGCGATAAGTCTGCTTACCGGTTTGGATCTCAAGACGATG 2412
5287 TTACCGGATTAAGCGCGAGCGGTTCGGCTGAAACCGGGGGTTCGTGCACACAGCCAGCTTG 5346
2413 TTACCGGATTAAGCGCGAGCGGTTCGGCTGAAACCGGGGGTTCGTGCACACAGCCAGCTTG 2472
5347 GAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGTGAATGAGAAAGCCACG 5406
2473 GAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGTGAATGAGAAAGCCACG 2532
5407 CTTCCGAAGGAGAAAGCGGACAGGATCCGTTAAGCGGAGGTTCGGAACGAGAGAG 5466
2533 CTTCCGAAGGAGAAAGCGGACAGGATCCGTTAAGCGGAGGTTCGGAACGAGAGAG 2592
5467 CGCAGAGGAGGCTTCCAGGGGGAACGCTGCTATCTTTATAGTCTCTGCGGTTTCG 5526
2593 CGCAGAGGAGGCTTCCAGGGGGAACGCTGCTATCTTTATAGTCTCTGCGGTTTCG 2652
5527 CACCTCTGACTTGAAGCTCGATTTTGTGATGCTCGTCAAGGGGGCGGAGCCTATGAAA 5586

2653 CACCTCTGACTTGAAGCTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAA 2712
5587 AACGCGAGAACCGCGCTTTTACGTTCCGTCCTTTTGTGCTGCTTTTGTCTACATG 5646
2713 AACGCGAGAACCGCGCTTTTACGTTCCGTCCTTTTGTGCTGCTTTTGTCTACATG 2772
5647 TTTCTTCTGCTGCTTATCCCTGATCTCTGGATAAACCGCTTATTTACCGCTTTGAGTGAGCT 5706
2773 TTTCTTCTGCTGCTTATCCCTGATCTCTGGATAAACCGCTTATTTACCGCTTTGAGTGAGCT 2832
5707 GATACCGCTTCGCGCAGCCGACGACGAGCGGAGCGAGTCACTGAGCGAGGAGCGGAA 5766
2833 GATACCGCTTCGCGCAGCCGACGACGAGCGGAGCGAGTCACTGAGCGAGGAGCGGAA 2892
5767 GAGCGCCCAATACGCAAAACCGCTCTCCCGCGCTTGGCCGATTCATTAATCGAG 5822
2893 GAGCGCCCAATACGCAAAACCGCTCTCCCGCGCTTGGCCGATTCATTAATCGAG 2948

RESULT 3
LOCUS AR037157 5534 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5801027.
ACCESSION AR037157
VERSION AR037157.1 GI:5955013
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5534)
AUTHORS Bennett M., May, S. and Ramsay, N.
TITLE Method of using transactivation proteins to control gene expression
JOURNAL in transgenic plants
Patent: US 5801027-A 3 01-SEP-1998;
FEATURES
Location/Qualifiers
1..5534
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 47.3%; Score 2755.6; DB 6; Length 5534;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2890; Conservative 0; Mismatches 38; Indels 74; Gaps 4;
Qy 2840 GATCGTTCAAACATTTGGCAATAAAGTTCTTAAGATTGAATCTGTGCGGCTCTCGG 2899
Db 2366 GATCGTTCAAACATTTGGCAATAAAGTTCTTAAGATTGAATCTGTGCGGCTCTCGG 2425
Qy 2900 ATGATTATCATATAATTTCTTGAATTAACGTTAAGCATGTAATAATTAACATGTAATGC 2959
Db 2426 ATGATTATCATATAATTTCTTGAATTAACGTTAAGCATGTAATAATTAACATGTAATGC 2485
Qy 2960 ATGAGTTTATTTAGATGGGTTTATGATTAAGTCCCGCAATTAATTAATTAATTAATAC 3019
Db 2486 ATGAGTTTATTTAGATGGGTTTATGATTAAGTCCCGCAATTAATTAATTAATTAATAC 2545
Qy 3020 CGGATAGAAAACAAATATAGCGCAAACTAGGATAAATTTATCGCGCGGCTGTCATCT 3079
Db 2546 CGGATAGAAAACAAATATAGCGCAAACTAGGATAAATTTATCGCGCGGCTGTCATCT 2605
Qy 3080 ATGTTACTAGATCGACC-----TGACGGCATGGGATCCGCGCGCCGATGC 3124
Db 2606 ATGTTACTAGATCGNNNNAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGG 2665
Qy 3125 GACGTCGCGGCCCAATTCGCCCTTATAGTGAGTGTATTAC---AATCTAGCCCGCTGTT 3181
Db 2666 GCGCCGGTACCAATTCGCCCTTATAGTGAGTGTATTACGCGCGCTCACTGCGCGCTGTT 2725
Qy 3182 TTACAACTGCTGAGTCTGGGAAAACCTGCGGTACCCACTTAATCGCCTTCAGCACAT 3241
Db 2726 TTACAACTGCTGAGTCTGGGAAAACCTGCGGTACCCACTTAATCGCCTTCAGCACAT 2785

QY 3242 CCCCCTTTGCGCAGCTGCGCTAATAGCGAAGAGCGCGCAGATCGCCCTTCCAAACAG 3301
DB 2786 CCCCCTTTGCGCAGCTGCGCTAATAGCGAAGAGCGCGCAGATCGCCCTTCCAAACAG 2845
QY 3302 TTGCGCAGCCTGAATGGCGAAT-GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGT 3360
DB 2846 TTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGT 2905
QY 3361 GTGCTGTGTAGCGCAGCGTGA CCGCTACACTTCCAGCGCCCTAGCGCGCCCTCCTTTC 3420
DB 2906 GTGCTGTGTAGCGCAGCGTGA CCGCTACACTTCCAGCGCCCTAGCGCGCCCTCCTTTC 2965
QY 3421 GCTTCTTCCCTTCTCTTCTCGCACGCTTCCGCGGCTTCCCGCTGAAGCTCTAAATCGG 3480
DB 2966 GCTTCTTCCCTTCTCTTCTCGCACGCTTCCGCGGCTTCCCGCTGAAGCTCTAAATCGG 3025
QY 3481 GGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTTACGGCACCTTCGACCCCAAAAACCTTGAT 3540
DB 3026 GGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTACGGCACCTTCGACCCCAAAAACCTTGAT 3085
QY 3541 TTGGGTGATGTTTCAAGTAGTGGGCATCGCCCTGTATAGACGGTTTTTCGCCCTTTGAAG 3600
DB 3086 TAGGGTGAATGGTTTCAAGTAGTGGGCATCGCCCTGTATAGACGGTTTTTCGCCCTTTGAAG 3145
QY 3601 TTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACCTCGAAACACCTCAACCT 3660
DB 3146 TTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACCTCGAAACACCTCAACCT 3205
QY 3661 ATCTCGGTCTAATCTTTTGTATTTAAGGATTTTTCGGGATTTTCGGCTATTTGGTTAAAA 3720
DB 3206 ATCTCGGTCTAATCTTTTGTATTTAAGGATTTTTCGGGATTTTCGGCTATTTGGTTAAAA 3265
QY 3721 AATGAGCTGATTTAAACAAATATTTAAGCGAATTTTAAACAAATATTTAAGCTTTTCAAT 3780
DB 3266 AATGAGCTGATTTAAACAAATATTTAAGCGAATTTTAAACAAATATTTAAGCTTTTCAAT 3325
QY 3781 TCGCCTGATCGCGTATTTCTCTTACGCTATCTGCGGTATTTTACACCGCATACAGT 3840
DB 3326 T-----AGST 3330
QY 3841 GGCACCTTTGCGGGAAATGTCGCGGAACCCCTATTGTTTATTTTCTAAATACATTTCA 3900
DB 3331 GGCACCTTTGCGGGAAATGTCGCGGAACCCCTATTGTTTATTTTCTAAATACATTTCA 3390
QY 3901 AATATGATCCGCTCATGAGCAATTAACCTCGATTAATGCTTCAATTAATTTGAAAGG 3960
DB 3391 AATATGATCCGCTCATGAGCAATTAACCTCGATTAATGCTTCAATTAATTTGAAAGG 3450
QY 3961 AAGATATGATTAATCAACATTTCCGTGTCGCCCTTATTTCCCTTTTTCGCCATTTTGC 4020
DB 3451 AAGATATGATTAATCAACATTTCCGTGTCGCCCTTATTTCCCTTTTTCGCCATTTTGC 3510
QY 4021 CTTCCTGTTTTCGTCACCCGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTG 4080
DB 3511 CTTCCTGTTTTCGTCACCCGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTG 3570
QY 4081 GGTGACAGTGGGTTCATCGAATCGATCTCAACAGCGGTGAAGATCCTTGAGAGTTTT 4140
DB 3571 GGTGACAGTGGGTTCATCGAATCGATCTCAACAGCGGTGAAGATCCTTGAGAGTTTT 3630
QY 4141 CGCCCCGAAGAACGTTTTCATGATGAGCACTTTTAAAGTTTCTCTATGTGGCGCGTA 4200
DB 3631 CGCCCCGAAGAACGTTTTCATGATGAGCACTTTTAAAGTTTCTCTATGTGGCGCGTA 3690
QY 4201 TTATCCCGTATTTAGCGCGGCAAGAGCAACTCGGTCCGCGCATACATTTCTCAGAA 4260
DB 3691 TTATCCCGTATTTAGCGCGGCAAGAGCAACTCGGTCCGCGCATACATTTCTCAGAA 3750
QY 4261 GACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCATCAGAGTAAGA 4320
DB 3751 GACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCATCAGAGTAAGA 3810
QY 4321 GAAATTATGAGTGTGCCATAACCATGAGTGATTAACACTGCGGCGCAACTTACTTCTGACA 4380

DB 3811 GAATTATGAGTGTGCCATAACCATGAGTGATTAACACTGCGGCGCACTTACTTCTGACA 3870
QY 4381 ACGATCGAGAGACCGAAGGAGCTAAACCGTTTTTTTGGCAACAATGCGGGGATCATGTAAT 4440
DB 3871 ACGATCGAGAGACCGAAGGAGCTAAACCGTTTTTTTGGCAACAATGCGGGGATCATGTAAT 3930
QY 4441 CGCCTTCTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGAGCGGTGACACC 4500
DB 3931 CGCCTTCTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGAGCGGTGACACC 3990
QY 4501 ACGATGCTGTAGCAATGGCAACAACCGTTGCGCAAACTATTAACTGCGCAACTACTTACT 4560
DB 3991 ACGATGCTGTAGCAATGGCAACAACCGTTGCGCAAACTATTAACTGCGCAACTACTTACT 4050
QY 4561 CTAGCTTCCCGGCAACAATTAATAGACTGATGAGCGCGATAAAGTTGAGGACCACTT 4620
DB 4051 CTAGCTTCCCGGCAACAATTAATAGACTGATGAGCGCGATAAAGTTGAGGACCACTT 4110
QY 4621 CTGCGCTCGGCCCTTCCGCGCTGCTGTTTATTTGCTGATAAATCTGAGCGCGGTAGCGT 4680
DB 4111 CTGCGCTCGGCCCTTCCGCGCTGCTGTTTATTTGCTGATAAATCTGAGCGCGGTAGCGT 4170
QY 4681 GGTCTCGCGGTATCATTTGCGACACTGCGGCCAGATGGTAAGCCCTCCCGTATTCGTAGTT 4740
DB 4171 GGTCTCGCGGTATCATTTGCGACACTGCGGCCAGATGGTAAGCCCTCCCGTATTCGTAGTT 4230
QY 4741 ATCTACAGCAGCGGGAGTCAGGCAACTATGATGAAACGAAATAGACAGATCGCTGAGATA 4800
DB 4231 ATCTACAGCAGCGGGAGTCAGGCAACTATGATGAAACGAAATAGACAGATCGCTGAGATA 4290
QY 4801 GGTCTCTCACTGATTAAGCAATTTGTAACCTGTCAGACCAAGTTTACTCATATATACTTTAG 4860
DB 4291 GGTCTCTCACTGATTAAGCAATTTGTAACCTGTCAGACCAAGTTTACTCATATATACTTTAG 4350
QY 4861 ATGATTTAAACTCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGTGATAAT 4920
DB 4351 ATGATTTAAACTCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGTGATAAT 4410
QY 4921 CTCATGACCAAAATCCCTTAAACGTGAGTTTTGTTCCACTGAGCGTCAGACCCGCTAGAA 4980
DB 4411 CTCATGACCAAAATCCCTTAAACGTGAGTTTTGTTCCACTGAGCGTCAGACCCGCTAGAA 4470
QY 4981 AAGATCAAAAGTCTTCTTGAGATCTCTTTTCTGCGGTAACTCTGCTCTGCAACA 5040
DB 4471 AAGATCAAAAGTCTTCTTGAGATCTCTTTTCTGCGGTAACTCTGCTCTGCAACA 4530
QY 5041 AAAAAACCAACCGCTACCGCGTGGTTTTGTTTGGCGGATCAAGAGCTACCAACTCTTTTT 5100
DB 4531 AAAAAACCAACCGCTACCGCGTGGTTTTGTTTGGCGGATCAAGAGCTACCAACTCTTTTT 4590
QY 5101 CCGAGGTAACTGCGTTTACGACAGCGCGAGATACCAATATACGTCTCTTAGTGAGCG 5160
DB 4591 CCGAGGTAACTGCGTTTACGACAGCGCGAGATACCAATATACGTCTCTTAGTGAGCG 4650
QY 5161 TAGTTAGCCCACTTCAAGAACTCTCTAGCACCGCTACATACCTCGCTCTGCTAATC 5220
DB 4651 TAGTTAGCCCACTTCAAGAACTCTCTAGCACCGCTACATACCTCGCTCTGCTAATC 4710
QY 5221 CTGTTACAGTGGCTGTGCGAGTGGGATTAAGTGTGTTTACCGGTTTGGACTCAAGA 5280
DB 4711 CTGTTACAGTGGCTGTGCGAGTGGGATTAAGTGTGTTTACCGGTTTGGACTCAAGA 4770
QY 5281 CGATAGTTTACCGGATTAAGCGCGAGCGGTGCGGCTGAACCGGGGTTTGTGACACAGCCC 5340
DB 4771 CGATAGTTTACCGGATTAAGCGCGAGCGGTGCGGCTGAACCGGGGTTTGTGACACAGCCC 4830
QY 5341 AGCTTGGAGCGAAACGACTTACACCGAACTGAGATACCTTACAGCTGAGCTATGAGAAAGC 5400
DB 4831 AGCTTGGAGCGAAACGACTTACACCGAACTGAGATACCTTACAGCTGAGCTATGAGAAAGC 4890
QY 5401 GCGACGCTTCCGAGGAGAAAGCGGACAGGTATCCGTTAAGCGGAGCGGTTCGGAACA 5460

```
Db 4891 GCCACGCTTCCGAGAGGAGAAAGCGGACAGGTATCCGGTAAGCGGACGGTTCGGAAACA 4950
QY 5461 GGAGAGCGCACGAGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCTGTFCGGG 5520
Db 4951 GGAGAGCGCACGAGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCTGTFCGGG 5010
QY 5521 TTTTGGCACCTCTGACTCTGAGCGTTCGATTTTGTGTAGTCTGTGAGGGGGGAGACCTTA 5580
Db 5011 TTTTGGCACCTCTGACTCTGAGCGTTCGATTTTGTGTAGTCTGTGAGGGGGGAGACCTTA 5070
QY 5581 TGGAAAAAGCCGACGAAACGGCGCTTTTACGCTTCTCGCCCTTTTGTGGCTTTTGTGCT 5640
Db 5071 TGGAAAAAGCCGACGAAACGGCGCTTTTACGCTTCTCGCCCTTTTGTGGCTTTTGTGCT 5130
QY 5641 CACATGTTCTTCTCGCTTATCCCTGATTTCTGTGTGAATAACCGTATTAACCGCTTTGAG 5700
Db 5131 CACATGTTCTTCTCGCTTATCCCTGATTTCTGTGTGAATAACCGTATTAACCGCTTTGAG 5190
QY 5701 TGAGCTGATACCGCTCGCCGACGCGAAACGACGAGGCGACGAGTCAGTGAGCGAGGAA 5760
Db 5191 TGAGCTGATACCGCTCGCCGACGCGAAACGACGAGGCGACGAGTCAGTGAGCGAGGAA 5250
QY 5761 GCGGACAGCGCCCAATACGAAACCGCTCTCCCGCGGTTGGCGGATTCATTAAATGC 5820
Db 5251 GCGGACAGCGCCCAATACGAAACCGCTCTCCCGCGGTTGGCGGATTCATTAAATGC 5310
QY 5821 AG 5822
Db 5311 AG 5312

RESULT 4
ARL12043
LOCUS ARL12043 5534 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6127606.
ACCESSION ARL12043
VERSION ARL12043.1 GI:12828891
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5534)
AUTHORS Bennett, M., May, S. and Ramsay, N.
TITLE Method of using transactivation proteins to control expression in transgenic plants
JOURNAL Patent: US 6127606-A 3 03-OCT-2000;
FEATURES
source Location/Qualifiers
1..5534
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 47.3%; Score 2755.6; DB 6; Length 5534;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2890; Conservative 0; Mismatches 38; Indels 74; Gaps 4;

QY 2840 GATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATTCCTGTTCGCGGCTTCGCG 2899
Db 2366 GATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATTCCTGTTCGCGGCTTCGCG 2425
QY 2900 ATGATTATCATATAATTTCTGTGTAATTAAGTAAAGCATGTAATTAATTAACATGTAATGC 2959
Db 2426 ATGATTATCATATAATTTCTGTGTAATTAAGTAAAGCATGTAATTAATTAACATGTAATGC 2485
QY 2960 ATGAGTTATTTATGAGATGGGTTTTTATGATTAGATGCCCGCAATTATACATTAAATAC 3019
Db 2486 ATGAGCTTATTTATGAGATGGGTTTTTATGATTAGATGCCCGCAATTATACATTAAATAC 2545
QY 3020 GCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAAATATTCGCGCGCGGTGTCACTC 3079
Db 2546 GCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAAATATTCGCGCGCGGTGTCACTC 2605
QY 3080 ATGTTACTAGATCGACC-----TGCAGGCATGGGATCCCGCGCGCATGC 3124
```

```
Db 2606 ATGTTACTAGATCNNGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGG 2665
QY 3125 GACGTCGGGCCCCAATTCGCCCTATAGTGAAGTGGTATTAC---AATTCACTGGCCGCTCGTT 3181
Db 2666 GCGCGGTTACCCAAATTCGCCCTATAGTGAAGTGGTATTACGCGCGCTCCTACCTGGCCGCTCGTT 2725
QY 3182 TTACACGTCGTGACTGGGAAACCTCGCGTTTACCAACTTAATCGCCTTGCGACACAT 3241
Db 2726 TTACACGTCGTGACTGGGAAACCTCGCGTTTACCAACTTAATCGCCTTGCGACACAT 2785
QY 3242 CCCCCCTTTCGCCAGCTGGCGTAAATAGCGAAGAGCCGCGACCGATCGCCTTCCCAACAG 3301
Db 2786 CCCCCCTTTCGCCAGCTGGCGTAAATAGCGAAGAGCCGCGACCGATCGCCTTCCCAACAG 2845
QY 3302 TTGCGCAGCTGAATGGCGAAT--GGACGCGCCCTGTAGGGCGCATTAAGCGCGGGGGT 3360
Db 2846 TTGCGCAGCTGAATGGCGAATGGGACGCGCCCTGTAGGGCGCATTAAGCGCGGGGGT 2905
QY 3361 GTGGTGGTTACGCGACGCTGACCGCTACACTTTGCCAGCGCCCTAGCGCCGCTCCTTTTC 3420
Db 2906 GTGGTGGTTACGCGACGCTGACCGCTACACTTTGCCAGCGCCCTAGCGCCGCTCCTTTTC 2965
QY 3421 GCTTTCTTCCCTTCTTCTCGCCAGCTTCGCGGCTTTCCCGTCAAGCTCTAAATCGG 3480
Db 2966 GCTTTCTTCCCTTCTTCTCGCCAGCTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGG 3025
QY 3481 GGGCTCCCTTTAGGTTCCGATTTAGAGCTTTAGGCACTTCGACCGCAAAAACCTTGAT 3540
Db 3026 GGGCTCCCTTTAGGTTCCGATTTAGTGTCTTACGGCACTTCGACCGCAAAAACCTTGAT 3085
QY 3541 TTGGGTGATGTTTACGCTAGTGGCCCATCGCCCTGATAGACGGTTTTTCGCTTTGACG 3600
Db 3086 TAGGTTGATGTTTACGCTAGTGGCCCATCGCCCTGATAGACGGTTTTTCGCTTTGACG 3145
QY 3601 TTGGAGTCCACGTTCTTTTAATAGTGGACTCTGTGTTCCAAAACCTGGAACAACTCAACCT 3660
Db 3146 TTGGAGTCCACGTTCTTTTAATAGTGGACTCTGTGTTCCAAAACCTGGAACAACTCAACCT 3205
QY 3661 ATCTCGGTCTATTTCTTTGATTTAAGGATTTTGGCGATTTTCGGCTATTGTTTAAAA 3720
Db 3206 ATCTCGGTCTATTTCTTTGATTTAAGGATTTTGGCGATTTTTCGGCTATTGTTTAAAA 3265
QY 3721 AATGAGCTGATTTAAACAAATTTAAACGCAATTTTAAACAAAATTTAAACGTTTACAAAT 3780
Db 3266 AATGAGCTGATTTAAACAAATTTTAAACGCAATTTTAAACAAAATTTTAAACGTTTACAAAT 3325
QY 3781 TCGGCTGATGCGGTATTTTCTCTTACGCACTCTGTGGGTAATTTCAACCGCATACAGGT 3840
Db 3326 T-----AGGT 3330
QY 3841 GGCACTTTTCGGGAAATGTGCGGACCGCTATTTGTTTATTTTCTTAATACATTCA 3900
Db 3331 GGCACTTTTCGGGAAATGTGCGGACCGCTATTTGTTTATTTTCTTAATACATTCA 3390
QY 3901 AATATGATCGCTCATGAGACAATTAACCTGATAAATGCTTCAATAATATTGAAAAAGG 3960
Db 3391 AATATGATCGCTCATGAGACAATTAACCTGATAAATGCTTCAATAATATTGAAAAAGG 3450
QY 3961 AAGAGTATGATTTCAAATTTCCGTGTCGCCCTTATTCCTTTTTCGGGCATTTTGC 4020
Db 3451 AAGAGTATGATTTCAAATTTCCGTGTCGCCCTTATTCCTTTTTCGGGCATTTTGC 3510
QY 4021 CTTCTGTTTTTGTCCACCGAAGACGCTGGTGAAGTAAAGATGCTGAGATCAGTTG 4080
Db 3511 CTTCTGTTTTTGTCCACCGAAGACGCTGGTGAAGTAAAGATGCTGAGATCAGTTG 3570
QY 4081 GGTGACAGAGTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCCTTGAGAGTTT 4140
Db 3571 GGTGACAGAGTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCCTTGAGAGTTT 3630
QY 4141 CCCCCCGAAGACGTTTTTCCCAATGATGAGCACTTTTAAAGTTCTCTATGTGCGCGGTA 4200
```

Db 3631 CGCCCCGAAGAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTA 3690
QY 4201 TTATCCCGTATGACCGCGGCAAGCAACTCGGTCCGCCATACACTATTCTCAGAAT 4260
Db 3691 TTATCCCGTATGACCGCGGCAAGCAACTCGGTCCGCCATACACTATTCTCAGAAT 3750
QY 4261 GACTTGGTTGAGTACTCACCAGTTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGA 4320
Db 3751 GACTTGGTTGAGTACTCACCAGTTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGA 3810
QY 4321 GAATATGCGTGTGTCATTAACCACTGATGATTAACACTGCGGCCAACTTACTTCTGACA 4380
Db 3811 GAATATGCGTGTGTCATTAACCACTGATGATTAACACTGCGGCCAACTTACTTCTGACA 3870
QY 4381 ACGATCGGAGACCGAAGAGAGCTAACCGCTTTTGTGACAACTATGAGGGATCATGTAACT 4440
Db 3871 ACGATCGGAGACCGAAGAGAGCTAACCGCTTTTGTGACAACTATGAGGGATCATGTAACT 3930
QY 4441 CGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACC 4500
Db 3931 CGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACC 3990
QY 4501 ACGATGCTGTAGCAATGGCAACCAACGTTGGCAAACTATTAACTGGCGCAACTACTTACT 4560
Db 3991 ACGATGCTGTAGCAATGGCAACCAACGTTGGCGCAAACTATTAACTGGCGCAACTACTTACT 4050
QY 4561 CTAGCTTCCCGGCAACCAATTAATAGACTGATGGAGCGCGATAAAGTTGACGACCACTT 4620
Db 4051 CTAGCTTCCCGGCAACCAATTAATAGACTGATGGAGCGCGATAAAGTTGACGACCACTT 4110
QY 4621 CTGCGCTCGGCCCTTCCGGCTGCTGCTTTTATGCTGATTAATCTGAGCGCGTGAGCGT 4680
Db 4111 CTGCGCTCGGCCCTTCCGGCTGCTGCTTTTATGCTGATTAATCTGAGCGCGTGAGCGT 4170
QY 4681 GGGTCTCGCGGTATCATTCAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATCTAGTT 4740
Db 4171 GGGTCTCGCGGTATCATTCAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATCTAGTT 4230
QY 4741 ATCTACACGACGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATA 4800
Db 4231 ATCTACACGACGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATA 4290
QY 4801 GGTGCTCTACTGATTAAGCAATGTAACGTGACGCCAAGTTTACTCATATATACTTTAG 4860
Db 4291 GGTGCTCTACTGATTAAGCAATGTAACGTGACGCCAAGTTTACTCATATATACTTTAG 4350
QY 4861 ATGATTTAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAAT 4920
Db 4351 ATGATTTAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAAT 4410
QY 4921 CTCATGACCAAAATCCCTTAACTGAGTTTTCCTGATGAGCGTCAGACCCCGTAGAA 4980
Db 4411 CTCATGACCAAAATCCCTTAACTGAGTTTTCCTGATGAGCGTCAGACCCCGTAGAA 4470
QY 4981 AAGATCAAAAGTCTTCTTGAGATCCCTTTTCTGCGGTATCTGCTGCTGCTGCAACA 5040
Db 4471 AAGATCAAAAGTCTTCTTGAGATCCCTTTTCTGCGGTATCTGCTGCTGCTGCAACA 4530
QY 5041 AAAAAACCAACGCTACACGCGTGTGTTTGGCGGATCAAGAGCTACCAACTCTTTT 5100
Db 4531 AAAAAACCAACGCTACACGCGTGTGTTTGGCGGATCAAGAGCTACCAACTCTTTT 4590
QY 5101 CCGAAGGTAACGCTTCCAGCAGCGGAGTACCAAAATACGTGCTCTTCTAGTGTAGCG 5160
Db 4591 CCGAAGGTAACGCTTCCAGCAGCGGAGTACCAAAATACGTGCTCTTCTAGTGTAGCG 4650
QY 5161 TAGTTAGGCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCGCTATC 5220
Db 4651 TAGTTAGGCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCGCTATC 4710
QY 5221 CTGTTACAGTGGCTGTGCCAGTGGCGATAGTCTGTCTTACCGGGTTGGACTCAAGA 5280
Db 4711 CTGTTACAGTGGCTGTGCCAGTGGCGATAGTCTGTCTTACCGGGTTGGACTCAAGA 4770

QY 5281 CGATAGTTACCGGATAAGGCGCAGCGTCCGGCTGAACGGGGGTTCTGTGCACACAGCCC 5340
Db 4771 CGATAGTTACCGGATAAGGCGCAGCGTCCGGCTGAACGGGGGTTCTGTGCACACAGCCC 4830
QY 5341 AGCTTGGAGCGAAGACCTTACACCGAACTGAGATACCTTACAGCGTGAAGTATGAGAAAGC 5400
Db 4831 AGCTTGGAGCGAAGACCTTACACCGAACTGAGATACCTTACAGCGTGAAGTATGAGAAAGC 4890
QY 5401 GCCACGCTTCCCGAAGGAGAAAGCGGATACCGTATCCGTTAAGCGGAGCGTCCGGAACA 5460
Db 4891 GCCACGCTTCCCGAAGGAGAAAGCGGATACCGTATCCGTTAAGCGGAGCGTCCGGAACA 4950
QY 5461 GGAGAGCGCAGGAGGAGCTTCCAGGGGAAAACGCTTCCAGGGGAAAACGCTTCCGTTGCTGCGG 5520
Db 4951 GGAGAGCGCAGGAGGAGCTTCCAGGGGAAAACGCTTCCGTTGCTGCGG 5010
QY 5521 TTTGCGCACCTCTGACTTGAAGCGTTCGATTTTGTGATGCTCGTCAGGGGCGGAGCCTA 5580
Db 5011 TTTGCGCACCTCTGACTTGAAGCGTTCGATTTTGTGATGCTCGTCAGGGGCGGAGCCTA 5070
QY 5581 TGGAAAACCGCAGCAGCGGCGCTTTTACGGTTCTGCGCTTTGCTGGCCTTTTGCT 5640
Db 5071 TGGAAAACCGCAGCAGCGGCGCTTTTACGGTTCTGCGCTTTTGCTGGCCTTTTGCT 5130
QY 5641 CACATGTTCTTCTGCTTATCCCTGTTATCCCTGATTCCTGTGATACCGTATTCAGCCTTTGAG 5700
Db 5131 CACATGTTCTTCTGCTTATCCCTGTTATCCCTGATTCCTGTGATACCGTATTCAGCCTTTGAG 5190
QY 5701 TGAGCTGATACCGCTCGCGCAGCCGAAACGACGAGCGAGCGAGTCACTGAGCGAGAA 5760
Db 5191 TGAGCTGATACCGCTCGCGCAGCCGAAACGACGAGCGAGCGAGTCACTGAGCGAGAA 5250
QY 5761 GCGGAGAGCGCCATACGAAACGCGCTCTCCCGCGGTTGGCGGATTCATTATGTC 5820
Db 5251 GCGGAGAGCGCCATACGAAACGCGCTCTCCCGCGGTTGGCGGATTCATTATGTC 5310
QY 5821 AG 5822
Db 5311 AG 5312

RESULT 5
AF173954/c

LOCUS AF173954 4350 bp DNA circular SYN 01-OCT-1999
DEFINITION Cloning vector pGEM-URA3, complete sequence.
ACCESSION AF173954
VERSION AF173954.1 GI:6002958
KEYWORDS Cloning vector pGEM-URA3
SOURCE Cloning vector pGEM-URA3
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4350)
AUTHORS Wilson,R.B., Davis,D. and Mitchell,A.P.
TITLE Rapid hypothesis testing with Candida albicans through gene disruption with short homology regions
J. Bacteriol. 181 (6), 1868-1874 (1999)
JOURNAL 99173911
MEDLINE 10074081
PUBMED 10074081
REFERENCE 2 (bases 1 to 4350)
AUTHORS Wilson,R.B., Davis,D. and Mitchell,A.P.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Microbiology, Columbia University, 701 W. 168th St., New York, NY 10032, USA
FEATURES
source location/Qualifiers
1..4350
/organism="Cloning vector pGEM-URA3"
/mol_type="genomic DNA"
/db_xref="taxon:101832"
/lab_host="Candida albicans SC5314"
/note="Candida albicans URA3 gene cloned into pGEM-T"
3409..4221
/gene="URA3"

gene

[illegible]

Db 1065 GCAACAAAAACACCGCTACACGCGTGGTGTGTTGTCGCGATCAAGAGCTACCAAC 1006
QY TCCTTTTCCGAAGTAACCTGCTTTCAGCAGAGCGCAGATACCAATACTGTCCTTCTAGT 5153
Db TCCTTTTCCGAAGTAACCTGCTTTCAGCAGAGCGCAGATACCAATACTGTCCTTCTAGT 946
QY GTAGCCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT 5213
Db GTAGCCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT 886
QY GCTAATCTGTACAGTGGTCTGCCAGTGGCGATAAGTCGTGCTTACCGGTTGGA 5273
Db GCTAATCTGTACAGTGGTCTGCCAGTGGCGATAAGTCGTGCTTACCGGTTGGA 826
QY CTCAGAAGCATAGTTACCGGATAGGCGCAGCGTCCGGCTGAAACGGGGGTTCTGTCAC 5333
Db CTCAGAAGCATAGTTACCGGATAGGCGCAGCGTCCGGCTGAAACGGGGGTTCTGTCAC 766
QY ACAGCCAGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATG 5393
Db ACAGCCAGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATG 706
QY AGAAGCGCAGCGCTTCCGAGGAGGAGGAGGCGCAGGTATCCGTTAAGCGCGAGGT 5453
Db AGAAGCGCAGCGCTTCCGAGGAGGAGGAGGCGCAGGTATCCGTTAAGCGCGAGGT 646
QY CGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGGAAACGCTGTGTATCTTTATAGTCC 5513
Db CGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGGAAACGCTGTGTATCTTTATAGTCC 586
QY TGTCGGGTTTCGCGACCTCTGACTGAGCGTGCATTTTGTGTATGCTCGTCAGGGGGGCG 5573
Db TGTCGGGTTTCGCGACCTCTGACTGAGCGTGCATTTTGTGTATGCTCGTCAGGGGGGCG 526
QY GAGCTATGGAAGACCGACGCGGCTTTTACGGTTCCTGCGCTTTTGTGCTGCTGCGCC 5633
Db GAGCTATGGAAGACCGACGCGGCTTTTACGGTTCCTGCGCTTTTGTGCTGCTGCGCC 466
QY TTTTGTGCATGTTCTTCTGCTGCTATCCCTGATTTCTGTGATACCGTATACCGC 5693
Db TTTTGTGCATGTTCTTCTGCTGCTATCCCTGATTTCTGTGATACCGTATACCGC 406
QY CTTTGTAGTGTATACCGCTGCGCGACGCGAAACGACGAGCGCAGTCAAGTGA 5753
Db CTTTGTAGTGTATACCGCTGCGCGACGCGAAACGACGAGCGCAGTCAAGTGA 346
QY CGAGGAGCGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGGTTGGCGGATCA 5813
Db CGAGGAGCGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGGTTGGCGGATCA 286
QY TTAATGCAG 5822
Db TTAATGCAG 277

RESULT 6
AF173955/c
LOCUS AF173955 5558 bp DNA circular SYN 01-OCT-1999
DEFINITION Cloning vector pGEM-HIS1, complete sequence.
ACCESSION AF173955
VERSION AF173955.1 GI:6002960
KEYWORDS Cloning vector pGEM-HIS1
SOURCE Cloning vector pGEM-HIS1
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 5558)
AUTHORS Wilson,R.B., Davis,D. and Mitchell,A.P.
TITLE Rapid hypothesis testing with candida albicans through gene
disruption with short homology regions
JOURNAL J. Bacteriol. 181 (6), 1868-1874 (1999)
MEDLINE 99173911
PUBMED 10074081

REFERENCE 2 (bases 1 to 5558)
AUTHORS Wilson,R.B., Davis,D. and Mitchell,A.P.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Microbiology, Columbia University, 701 W.
168th St., New York, NY 10032, USA
FEATURES
source
1. 5558
/organism="Cloning vector pGEM-HIS1"
/mol_type="genomic DNA"
/db_xref="taxon:101833"
/lab_hosts="Candida albicans SC5314"
/notes="Candida albicans HIS1 gene into pGEM-T"
2980. 5558
/gene="HIS1"
3514. 4410
/gene="HIS1"
/codon_start=1
/product="ATP phosphoribosyltransferase"
/protein_id="AAF00227.1"
/db_xref="GI:6002961"
translations="MDLVNHLPLRLFAVPKGRLYEKCNCNLLSGADIOPRRSNRLDI
ALSTNLPALIFLPAADI PVFVGEKNCDLGITGLDOI KEAEPDNIEDLIDLKFGSK
LQIQVPADGEYEPQELVKKIVSFTKLSTIDFKQLSDRPTNIRYVGGVSVEASCALG
VADAVDLVESGTMKAAGLKALETIDETSAHLISSKSKPPEWNVIIYVRLQGVLLAA
QEVLCNYPAPKSIQAKCTITTPGRRATVSTLDKHSDDDEEDWVAISSMYNRKEIGNV
MDLKKAGATDILVLEISRCRV"
ORIGIN
Query Match 46.5%; Score 2705.8; DB 12; Length 5558;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2707; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 CGCGCGCATCGCAGCTCGGCCCAATTCGCCCTATAGTAGTGTATTAACAATTCACCTGG 3173
Db |||||
QY 2960 CGGAGCATCGCAGCTCGGCCCAATTCGCCCTATAGTAGTGTATTAACAATTCACCTGG 2901
Db |||||
QY 3174 CGTCGTTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACTTAATCGCCTTG 3233
Db |||||
QY 2900 CGTCGTTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACTTAATCGCCTTG 2841
Db |||||
QY 3234 CAGCATCCCCCTTCGCCAGCTGGCGTAATAGCAGAGGCGCCGACCGATCGCCCTT 3293
Db |||||
QY 2840 CAGCATCCCCCTTCGCCAGCTGGCGTAATAGCAGAGGCGCCGACCGATCGCCCTT 2781
Db |||||
QY 3294 CCCAACAGTTGCGCAGCCTGAATGGCGAATGGAGCGGCCCTGTAGCGCGCATTAAGCGC 3353
Db |||||
QY 2780 CCCAACAGTTGCGCAGCCTGAATGGCGAATGGAGCGGCCCTGTAGCGCGCATTAAGCGC 2721
Db |||||
QY 3354 GCGGCTGTGGTGTGTTACGCGCAGCGTGACCGCTACATTTGCCAGCGCCCTAGCGCCCGC 3413
Db |||||
QY 2720 GCGGCTGTGGTGTGTTACGCGCAGCGTGACCGCTACATTTGCCAGCGCCCTAGCGCCCGC 2661
Db |||||
QY 3414 TCCTTTTCGCTTTCTTCCTTCCTTTCTCGCCAGCTTCGCGGCTTTCCCGTCAAGCTCT 3473
Db |||||
QY 2660 TCCTTTTCGCTTTCTTCCTTCCTTTCTCGCCAGCTTCGCGGCTTTCCCGTCAAGCTCT 2601
Db |||||
QY 3474 AAATCGGGGCTCCCTTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAA 3533
Db |||||
QY 2600 AAATCGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAA 2541
Db |||||
QY 3534 ACTTGATTTGGGTGATGGTTACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCC 3593
Db |||||
QY 2540 ACTTGATTTGGGTGATGGTTACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCC 2481
Db |||||
QY 3594 TTTGAGCTTGGAGTCCACGTTCTTTTAATAGTGACCTTTGTTCCAACTGGACACACT 3653
Db |||||
QY 2480 TTTGAGCTTGGAGTCCACGTTCTTTTAATAGTGACCTTTGTTCCAACTGGACACACT 2421
Db |||||
QY 3654 CAACCTATCTCGGTCTATTTCTTTGATTATAAGGGATTTTCGGATTTTCGGCTATTG 3713
Db |||||
QY 2420 CAACCTATCTCGGTCTATTTCTTTGATTATAAGGGATTTTCGGATTTTCGGCTATTG 2361
Db |||||
QY 3714 GTTAAANAATGAGCTGATTTTAAACGAATTTTAAACGAATTTTAAACGAATTTAAGCTT 3773
Db |||||

Db ||||| 2360 GTTAAAAATGAGCTGATTTAAACAAATATTAAACGGAATTTAAACAAATATTAAACGTT 2301
Qy ||||| 3774 TACAATTTTCGCTGATGCGGTATTTTCTCTTACGATCTGTCGGTATTTTACACCGCA 3833
Db ||||| 2300 TACAATTTTCGCTGATGCGGTATTTTCTCTTACGATCTGTCGGTATTTTACACCGCA 2241
Qy ||||| 3834 TACAGGTGGCATTCTTTCGGGGAAATGTCGGGAAACCCCTATTCTTTTATTTTCTAAAT 3893
Db ||||| 2240 TACAGGTGGCATTCTTTCGGGGAAATGTCGGGAAACCCCTATTCTTTTATTTTCTAAAT 2181
Qy ||||| 3894 ACATTCAAAATATGATTCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTG 3953
Db ||||| 2180 ACATTCAAAATATGATTCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTG 2121
Qy ||||| 3954 AAAAGGAAGATGATGAGTATTTCAACATTTCCGTCGTCGCCCTTATTCCCTTTTTCGGGC 4013
Db ||||| 2120 AAAAGGAAGATGATGAGTATTTCAACATTTCCGTCGTCGCCCTTATTCCCTTTTTCGGGC 2061
Qy ||||| 4014 ATTTCGCTTCTCTGTTTTGCTCACCCGAAACGCTGGTGAAGTAAAGATGCTGAAGA 4073
Db ||||| 2060 ATTTCGCTTCTCTGTTTTGCTCACCCGAAACGCTGGTGAAGTAAAGATGCTGAAGA 2001
Qy ||||| 4074 TCAGTTGGGTGACGAGTGGGTATCATCGAATCTGATCTCAACAGCGGTAAAGATCCTTGA 4133
Db ||||| 2000 TCAGTTGGGTGACGAGTGGGTATCATCGAATCTGATCTCAACAGCGGTAAAGATCCTTGA 1941
Qy ||||| 4134 GAGTTTTCCGCCGGAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTG 4193
Db ||||| 1940 GAGTTTTCCGCCGGAAGAGCTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTG 1881
Qy ||||| 4194 CGCGGTATTATCCGTAATTGACCGCGGGAAGAGCAACTCGGTGCGCGCATACACTATTC 4253
Db ||||| 1880 CGCGGTATTATCCGTAATTGACCGCGGGAAGAGCAACTCGGTGCGCGCATACACTATTC 1821
Qy ||||| 4254 TCAGATGACTTGGTTGAGTACTCAACGATCAGAAAAGCACTTACGGATGCGCATGAC 4313
Db ||||| 1820 TCAGATGACTTGGTTGAGTACTCAACGATCAGAAAAGCACTTACGGATGCGCATGAC 1761
Qy ||||| 4314 AGTAAGAGATTTATGAGTGTCTGCTCAATGAGTAAACATGAGTAAACACTCGCGCCCACTTACT 4373
Db ||||| 1760 AGTAAGAGATTTATGAGTGTCTGCTCAATGAGTAAACATGAGTAAACACTCGCGCCCACTTACT 1701
Qy ||||| 4374 TCTGACAAACGATCGAGGACCGAAGGAGCTAAACCGCTTTTTCGCAAAATGCGGGATCA 4433
Db ||||| 1700 TCTGACAAACGATCGAGGACCGAAGGAGCTAAACCGCTTTTTCGCAAAATGCGGGATCA 1641
Qy ||||| 4434 TGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 4493
Db ||||| 1640 TGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 1581
Qy ||||| 4494 TGACACACGATGCTGTAGCAATGGCAACCACTGCGCAAACTATTAACTGCGCACT 4553
Db ||||| 1580 TGACACACGATGCTGTAGCAATGGCAACCACTGCGCAAACTATTAACTGCGCACT 1521
Qy ||||| 4554 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGAGTGAAGCGGATTAAGTTGCGAG 4613
Db ||||| 1520 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGAGTGAAGCGGATTAAGTTGCGAG 1461
Qy ||||| 4614 ACCACTTCGCTGCGCCCTTCGGCTGGCTGCTGTTTATTCGTGATAATCTGGAGCCGG 4673
Db ||||| 1460 ACCACTTCGCTGCGCCCTTCGGCTGGCTGCTGTTTATTCGTGATAATCTGGAGCCGG 1401
Qy ||||| 4674 TGAGCGTGGTCTCGCGTATCATTTGACAGCTGGGGCAGATGTTAAGCCCTCCCGTAT 4733
Db ||||| 1400 TGAGCGTGGTCTCGCGTATCATTTGACAGCTGGGGCAGATGTTAAGCCCTCCCGTAT 1341
Qy ||||| 4734 CGTAGTTATCAACGACGCGGAGTCAGGCAACTATGATGAACGAAATAGACATGCG 4793
Db ||||| 1340 CGTAGTTATCAACGACGCGGAGTCAGGCAACTATGATGAACGAAATAGACATGCG 1281
Qy ||||| 4794 TCAGATAGGTGCTCACTGATTAAGCAATGGTAACTGTCAGACCAAGTTTACTCATATAT 4853

RESULT 7
E63777/c

Db ||||| 1280 TGAGATAGGTGCTCACTGATTAAGCAATGTAACCTGTGACACCAAGTTTACTCATATAT 1221
Qy ||||| 4854 ACTTTAGATTCATTTTAAACCTTTCAATTTTAAATTTAAAGAGTCTAGTGAAGATCCTTTT 4913
Db ||||| 1220 ACTTTAGATTCATTTTAAACCTTTCAATTTTAAATTTAAAGAGTCTAGTGAAGATCCTTTT 1161
Qy ||||| 4914 TGATAATCTCATGACCAAAATCCCTTAAACGTGAGTTCCTTTCCTGATCTGAGGTGAGACCC 4973
Db ||||| 1160 TGATAATCTCATGACCAAAATCCCTTAAACGTGAGTTCCTTTCCTGATCTGAGGTGAGACCC 1101
Qy ||||| 4974 CGTAAAGATCAAAAGATCTTCTTGATGATCTTTTCTGCGCTAAATCTGCTGCTT 5033
Db ||||| 1100 CGTAAAGATCAAAAGATCTTCTTGATGATCTTTTCTGCGCTAAATCTGCTGCTT 1041
Qy ||||| 5034 GCMAACAAAAAACCAACCGCTACCAAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAAC 5093
Db ||||| 1040 GCMAACAAAAAACCAACCGCTACCAAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAAC 981
Qy ||||| 5094 TCTTTTTCGAAAGGTAACTGGCTTCAGCAGAGCGGAGATACCAATATCTGCTCTTACT 5153
Db ||||| 980 TCTTTTTCGAAAGGTAACTGGCTTCAGCAGAGCGGAGATACCAATATCTGCTCTTACT 921
Qy ||||| 5154 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCTTACATACCTGCTCT 5213
Db ||||| 920 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCTTACATACCTGCTCT 861
Qy ||||| 5214 GCTAACTCTGTTACAGTGGCTGCTGCGGATGCGGATTAAGTCTGTTTACCGGGTTGGA 5273
Db ||||| 860 GCTAACTCTGTTACAGTGGCTGCTGCGGATGCGGATTAAGTCTGTTTACCGGGTTGGA 801
Qy ||||| 5274 CTCAAGACGATAGTTACCGGATAAGCGGAGCGGTCGGGTGAAACCGGGGGTTCTGTCAC 5333
Db ||||| 800 CTCAAGACGATAGTTACCGGATAAGCGGAGCGGTCGGGTGAAACCGGGGGTTCTGTCAC 741
Qy ||||| 5334 ACAGCCAGCTTGGAGGGAACGACTACACCGAACTCTGAGTACCTACAGCGTCTGAGTATG 5393
Db ||||| 740 ACAGCCAGCTTGGAGGGAACGACTACACCGAACTCTGAGTACCTACAGCGTCTGAGTATG 681
Qy ||||| 5394 AGAAGCGCCACCTTCCGAGGGGAAAGCGGACAGGATCCGGTAAAGCGGACAGGT 5453
Db ||||| 680 AGAAGCGCCACCTTCCGAGGGGAAAGCGGACAGGATCCGGTAAAGCGGACAGGT 621
Qy ||||| 5454 CGAAACAGGAGAGCGACGAGGGAGCTTCCAGGGGAAACGCGTGTATCTTTATAGTCC 5513
Db ||||| 620 CGAAACAGGAGAGCGACGAGGGAGCTTCCAGGGGAAACGCGTGTATCTTTATAGTCC 561
Qy ||||| 5514 TGTGCGGTTTCGCCACCTCTGACTTGGAGCTGCAATTTTGTGATGCTGCTGAGGGGCG 5573
Db ||||| 560 TGTGCGGTTTCGCCACCTCTGACTTGGAGCTGCAATTTTGTGATGCTGCTGAGGGGCG 501
Qy ||||| 5574 GAGCCTATGAAACCAACCGCAGCAGCGGCTTTTACGGTTCTGCGCTTTTCTGCGCC 5633
Db ||||| 500 GAGCCTATGAAACCAACCGCAGCAGCGGCTTTTACGGTTCTGCGCTTTTCTGCGCC 441
Qy ||||| 5634 TTTTGTCTCACATGTTCTTCTGCGTTATCCCTGATTTCTGAGTAAACCGTATTTACCGC 5693
Db ||||| 440 TTTTGTCTCACATGTTCTTCTGCGTTATCCCTGATTTCTGAGTAAACCGTATTTACCGC 381
Qy ||||| 5694 CTTTGTGAGTGAATACCGCTCCCGCAGCGGAAACCGCAGCGGAGTCAAGTCAAGTCCG 5753
Db ||||| 380 CTTTGTGAGTGAATACCGCTCCCGCAGCGGAAACCGCAGCGGAGTCAAGTCAAGTCCG 321
Qy ||||| 5754 CGAGGAGCGGAGGCGCCCAATACGAAACCGGCTCTCCCGCGGCTTCCCGCGGATTC 5813
Db ||||| 320 CGAGGAGCGGAGGCGCCCAATACGAAACCGGCTCTCCCGCGGCTTCCCGCGGATTC 261
Qy ||||| 5814 TTAATGCGAG 5822
Db ||||| 260 TTAATGCGAG 252

LOCUS	E63777	4229 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION	Method for assaying the stability of genetic information in animal cells.					
ACCESSION	E63777					
VERSION	E63777.1	GI:22553615				
KEYWORDS	JP 2001087000-A/5.					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1 (bases 1 to 4229)					
AUTHORS	Nakanishi,M. and Ikawa,Y.					
TITLE	Method for assaying the stability of genetic information in animal					
JOURNAL	Patent: JP 2001087000-A 5 03-APR-2001;					
COMMENT	KK SENTAN KAGAKU GIJUTSU INCUBATION CENTER OS Artificial Sequence PN JP 2001087000-A/5 PD 03-APR-2001 PI 17-SEP-1999 JP 1999264320 PL MASATO NAKANISHI,YUMI IKAWA PC C12Q1/68,C12N15/10,C12N15/09,A61K48/00,C12N5/00, PC C12N15/00 CC Restriction enzyme BamHI-cut site CC Restriction enzyme SmaI-cut site FH Key Location/Qualifiers. FEATURES source 1..4229 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"					
ORIGIN						
Query Match	46.1%; Score 2686; DB 6; Length 4229;					
Best Local Similarity	100.0%; Pred. No. 0;					
Matches 2686;	Conservative	0;	Mismatches	0;	Gaps	0;
QY	3137	AATTGCGCCTTAGTGAGTCGTATTCAATCTACTGGCGTGGTCTTTTACAAGCTGTGCAC	3196			
DB	3157	AATTGCGCCTTAGTGAGTCGTATTCAATCTACTGGCGTGGTCTTTTACAAGCTGTGCAC	3098			
QY	3197	TGGGAACCCCTGGCGTTACCACAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGC	3256			
DB	3097	TGGGAACCCCTGGCGTTACCACAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGC	3038			
QY	3257	TGGGTTAATAGCAAGAGCCCGCACCGATCGCCCTTCCCACAGTTGCGAGCTCGAAT	3316			
DB	3037	TGGGCGTAATAGCAAGAGCCCGCACCGATCGCCCTTCCCACAGTTGCGAGCTCGAAT	2978			
QY	3317	GGCGAATGACGGCCCTGTAGCGGGCAATTAGCGCGCGGGTGTGTGTTACGGCA	3376			
DB	2977	GGCGAATGACGGCCCTGTAGCGGGCAATTAGCGCGCGGGTGTGTGTTACGGCA	2918			
QY	3377	GGGTGACCGCTACATTGCGACGGCCCTAGCGCCCGCTTTCGCTTCTTCCTTCCTTCCT	3436			
DB	2917	GGGTGACCGCTACATTGCGACGGCCCTAGCGCCCGCTTTCGCTTCTTCCTTCCTTCCT	2858			
QY	3437	TTCTCGCAGCTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGT	3496			
DB	2857	TTCTCGCAGCTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGT	2798			
QY	3497	TCCGATTTAGACCTTTAGGGACCTCGACCGCAAAAACCTTGATTTGGGTGATGGTTTCA	3556			
DB	2797	TCCGATTTAGACCTTTAGGGACCTCGACCGCAAAAACCTTGATTTGGGTGATGGTTTCA	2738			
QY	3557	GTAGTGGGCCATTGCGCCCTGTAGACGGTTTTTCGCCCTTTGACGTTGAGTCCACGTTCT	3616			
DB	2737	GTAGTGGGCCATTGCGCCCTGTAGACGGTTTTTCGCCCTTTGAGTCCACGTTCT	2678			
QY	3617	TTAATAAGTCGACTCTGTGTCCAACCTGGAACAACTCAACCTTATCTCGGTCTATTCTT	3676			
DB	2677	TTAATAAGTCGACTCTGTGTCCAACCTGGAACAACTCAACCTTATCTCGGTCTATTCTT	2618			
QY	3677	TTGATTTATAAGGGATTTTGCAGATTTTCGGCTATTGTTAAAAAATGACCTGATTTAAC	3736			

QY	4817	AGCATTTGTAACGTGTCAGACCAAGTTTACTCATATATATACCTTTAGATTGATTTAAACTTC	4876
Db	1477	AGCATTTGTAACGTGTCAGACCAAGTTTACTCATATATATACCTTTAGATTGATTTAAACTTC	1418
QY	4877	ATTTTAAATTTAAAGATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCC	4936
Db	1417	ATTTTAAATTTAAAGATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCC	1358
QY	4937	CTTAAAGTGAAGTTTCCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAAGGATCTT	4996
Db	1357	CTTAAAGTGAAGTTTCCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAAGGATCTT	1298
QY	4997	CTTGAGATCTTTTCTCGGGTAATCTGCTGCTTGGAACCAAAAACCCACCGCTAC	5056
Db	1297	CTTGAGATCTTTTCTCGGGTAATCTGCTGCTTGGAACCAAAAACCCACCGCTAC	1238
QY	5057	CAGGGTGGTTTGTTCGCGGATCAAGACTACCACTCTTTTTCGAAAGTAACTGGCT	5116
Db	1237	CAGGGTGGTTTGTTCGCGGATCAAGACTACCACTCTTTTTCGAAAGTAACTGGCT	1178
QY	5117	TCAGCAGAGCGCATACCAAAATCTCTCTTCTAGTGTAGCCGTAGTTAGGCCACCACT	5176
Db	1177	TCAGCAGAGCGCATACCAAAATCTCTCTTCTAGTGTAGCCGTAGTTAGGCCACCACT	1118
QY	5177	TCAGAAACTCTGTAGACCGGCTACATACCTCGCTCTGCTAATCTGTTACCAGTGGCTG	5236
Db	1117	TCAGAAACTCTGTAGACCGGCTACATACCTCGCTCTGCTAATCTGTTACCAGTGGCTG	1058
QY	5237	CTGCCAGTGGGATAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTTACCGGATA	5296
Db	1057	CTGCCAGTGGGATAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTTACCGGATA	998
QY	5297	AGGCGCAGCGGTCCGGCTGAAACGGGGGGTTTCTGTACACACAGCCAGCTTGGAGCGAACGA	5356
Db	997	AGGCGCAGCGGTCCGGCTGAAACGGGGGGTTTCTGTACACACAGCCAGCTTGGAGCGAACGA	938
QY	5357	CCTACACCGAACTCAGATACCTACAGCGTGAGCTATAGAAAGCGCCACGCTTCCGAG	5416
Db	937	CCTACACCGAACTCAGATACCTACAGCGTGAGCTATAGAAAGCGCCACGCTTCCGAG	878
QY	5417	GGAGAAAGCGGACAGGTATCCGTTACGGCAGGGTCGGAACAGGAGAGCGACGAGGG	5476
Db	877	GGAGAAAGCGGACAGGTATCCGTTACGGCAGGGTCGGAACAGGAGAGCGACGAGGG	818
QY	5477	AGCTTCCAGGGGAAACCGCTTGTATCTTTATAGTCTCTGTCGGGTTCCGCCACCTCTGAC	5536
Db	817	AGCTTCCAGGGGAAACCGCTTGTATCTTTATAGTCTCTGTCGGGTTCCGCCACCTCTGAC	758
QY	5537	TTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCGCTATGAAAACCGCAGCA	5596
Db	757	TTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCGCTATGAAAACCGCAGCA	698
QY	5597	ACGGGCTTTTACGGTTCTGGCTTTTGTGCTGGCTTTTGTCTCACATGTTCTTCTCTG	5656
Db	697	ACGGGCTTTTACGGTTCTGGCTTTTGTGCTGGCTTTTGTCTCACATGTTCTTCTCTG	638
QY	5657	CGTTATCCCTGATTTCTGTGGATAACCGTATTTACCGCCCTTTTGTGAGTGTATACCGCTC	5716
Db	637	CGTTATCCCTGATTTCTGTGGATAACCGTATTTACCGCCCTTTTGTGAGTGTATACCGCTC	578
QY	5717	GCCGAGCGGAAACGACCGAGCGACGAGTCACTGAGCGAGGAGCGGAGAGCGGCCCAA	5776
Db	577	GCCGAGCGGAAACGACCGAGCGACGAGTCACTGAGCGAGGAGCGGAGAGCGGCCCAA	518
QY	5777	TACGAAACCGCTCTCCCGCGCTTGGCGGATTTGCGGATTCATTAATGACG	5822
Db	517	TACGAAACCGCTCTCCCGCGCTTGGCGGATTTGCGGATTCATTAATGACG	472

DEFINITION Sequence 6 from Patent W002086100.
ACCESSION AX590988
VERSION AX590988.1 GI:27949532
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bosman,A., Depla,E., Deschamps,G., Sablon,E., Samson,I., van Broekhoven,A. and Haelewyn,J.
TITLE Expression of core-glycosylated hcv envelope proteins in yeast
JOURNAL Patent: WO 02086100-A 6 31-OCT-2002;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
1..3448
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="vector pGEMTE1sh6"

ORIGIN	Query Match	46.1%;	Score 2683.4;	DB 6;	Length 3448;
	Best Local Similarity	99.4%;	Pred. No. 0;		
	Matches 2693;	Conservative	0;	Mismatches	16;
				Indels	0;
QY	3114	CGCGCGCATCGGACGTGCGGCCCAATTCGCCCTATAGTGTAGTTCGTAATTAACAATTCACCTGG	3173		
Db	2985	CGGAGCATCGGACGTGCGGCCCAATTCGCCCTATAGTGTAGTTCGTAATTAACAATTCACCTGG	2926		
QY	3174	CCGTCGTTTTACAAACGTCGTGACTGGGAAAACCCCTGCGGTACCCAACTTAATCGCCTTG	3233		
Db	2925	CCGTCGTTTTACAAACGTCGTGACTGGGAAAACCCCTGCGGTACCCAACTTAATCGCCTTG	2866		
QY	3234	CAGCACATCCCCCTTTCCGACGCTGGCGTAAATAGCGAAGAGGCCGCGACGATCGCCCTT	3293		
Db	2865	CAGCACATCCCCCTTTCCGACGCTGGCGTAAATAGCGAAGAGGCCGCGACGATCGCCCTT	2806		
QY	3294	CCCAACAGTTGCGCAGCGCTGAATCGCGAATGAGCGCGCCCTGTAGCGCGCATTAAGCGC	3353		
Db	2805	CCCAACAGTTGCGCAGCGCTGAATCGCGAATGAGCGCGCCCTGTAGCGCGCATTAAGCGC	2746		
QY	3354	GGCGGGTGTGTGGTTTACGGCGCAGCGCTGACCGCTTACCTTCCAGCGCCCTTAGCGCCCGC	3413		
Db	2745	GGCGGGTGTGTGGTTTACGGCGCAGCGCTGACCGCTTACCTTCCAGCGCCCTTAGCGCCCGC	2686		
QY	3414	TCCCTTCGCTTTCTTCCCTTCTTCGCGACGCTTCCCGCGCTTCCCGCTCAGCTCT	3473		
Db	2685	TCCCTTCGCTTTCTTCCCTTCTTCGCGACGCTTCCCGCGCTTCCCGCTCAGCTCT	2626		
QY	3474	AAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTAGCGACCTTCGACCGCAAAA	3533		
Db	2625	AAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTAGCGACCTTCGACCGCAAAA	2566		
QY	3534	ACTTGATTTGGGTGATGGTTCACGCTAGTGGGCCATCGCCCTGTAGACGGTTTTTCGCC	3593		
Db	2565	ACTTGATTTGGGTGATGGTTCACGCTAGTGGGCCATCGCCCTGTAGACGGTTTTTCGCC	2506		
QY	3594	TTTGACGTTGGAGTCCAGGTTCTTTATAGTGGACTCTTGTTCMAACTGGAACACACT	3653		
Db	2505	TTTGACGTTGGAGTCCAGGTTCTTTTAAATAGTGGACTCTTGTTCMAACTGGAACACACT	2446		
QY	3654	CAACCCCTATCTCGGCTATCTTTTGAATTAAGGATTTTCCGATTTCCGCGCTATTG	3713		
Db	2445	CAACCCCTATCTCGGCTATCTTTTGAATTAAGGATTTTCCGATTTCCGCGCTATTG	2386		
QY	3714	GTTAAAAAATGAGCTGATTTAAACAAATTTTAAACGGAATTTTAAACAAATATTACGTT	3773		
Db	2385	GTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGGAATTTTAAACAAATATTACGTT	2326		
QY	3774	TACAAATTCGCGCTGATCGGATTTTCTCCTTACGATCTGTGGGTTATTCACACCGCA	3833		
Db	2325	TACAAATTCGCGCTGATCGGATTTTCTCCTTACGATCTGTGGGTTATTCACACCGCA	2266		

QY 3834 TACAGTGGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 3893
Db 2265 TACAGGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 2206
QY 3894 ACATTCAAAATATGATCGCTCATGAGACAAATAACCTGTAAATGCTTCAATAATATTG 3953
Db 2205 ACATTCAAAATATGATCGCTCATGAGACAAATAACCTGTAAATGCTTCAATAATATTG 2146
QY 3954 AAAAGGAAGATGATGATTTCAACATTTCCGTTGCGCCCTTATCCCTTTTGTGGCG 4013
Db 2145 AAAAGGAAGATGATGATTTCAACATTTCCGTTGCGCCCTTATCCCTTTTGTGGCG 2086
QY 4014 ATTTTGCCTTCCCTTTTTCCTTACCCGAGAAACGCTGGTGAAGTAAAGTGTGAAGA 4073
Db 2085 ATTTTGCCTTCCCTTTTTCCTTACCCGAGAAACGCTGGTGAAGTAAAGTGTGAAGA 2026
QY 4074 TCAGTTGGGTGACAGTGGTGTACATCGAACTGATCTCAACAGCGGTAAAGTCTTGA 4133
Db 2025 TCAGTTGGGTGACAGTGGTGTACATCGAACTGATCTCAACAGCGGTAAAGTCTTGA 1966
QY 4134 GAGTTTTCGCGGAGAAAGCTTTTCCATGATGAGCACTTTTAAAGTTCTGCTATGTC 4193
Db 1965 GAGTTTTCGCGGAGAAAGCTTTTCCATGATGAGCACTTTTAAAGTTCTGCTATGTC 1906
QY 4194 CGCGGTATTTATCCGTTATTCACGCGGCGGAGAGCACTCGTCCGCGATACACTATTC 4253
Db 1905 TACACTATTTATCCGTTATTCACGCGGCGGAGAGCACTCGTCCGCGGCGGTATTC 1846
QY 4254 TCAGATGACTTGGTTGAGTACTCACCAAGTCAAGAAAGCATCTTACGGATGCGATGAC 4313
Db 1845 TCAGATGACTTGGTTGAGTACTCACCAAGTCAAGAAAGCATCTTACGGATGCGATGAC 1786
QY 4314 AGTAAGAAATTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4373
Db 1785 AGTAAGAAATTTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1726
QY 4374 TCTGACAAAGATCGGAGGACCGAAGGAGCTAAACGGCTTTTGTGCAACATGGGGATCA 4433
Db 1725 TCTGACAAAGATCGGAGGACCGAAGGAGCTAAACGGCTTTTGTGCAACATGGGGATCA 1666
QY 4434 TGTAATCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4493
Db 1665 TGTAATCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606
QY 4494 TGACACAGATGCTGTGAGCAATGCAACAGCTTGGCGAACTATTAACTGGCGAACT 4553
Db 1605 TGACACAGATGCTGTGAGCAATGCAACAGCTTGGCGAACTATTAACTGGCGAACT 1546
QY 4554 ACTTACTAGCTTCCGCGCAAAATTAATAGATCGATGAGGCGGATAAGTTGACGG 4613
Db 1545 ACTTACTAGCTTCCGCGCAAAATTAATAGATCGATGAGGCGGATAAGTTGACGG 1486
QY 4614 ACCACTTTCGCTCGGCGCTTCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4673
Db 1485 ACCACTTTCGCTCGGCGCTTCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1426
QY 4674 TGAGCTGGGTTCGCGGTATCATTTGAGCACTTGGGCGCAGATGGTAAGCCCTCCCGTAT 4733
Db 1425 TGAGCTGGGTTCGCGGTATCATTTGAGCACTTGGGCGCAGATGGTAAGCCCTCCCGTAT 1366
QY 4734 CGTAGTTATCTACAGCGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC 4793
Db 1365 CGTAGTTATCTACAGCGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC 1306
QY 4794 TGAGATGAGTGCCTCACTGATTAAGCAATGGTAACCTGTGAGACCAAGTTTACTCATATAT 4853
Db 1305 TGAGATGAGTGCCTCACTGATTAAGCAATGGTAACCTGTGAGACCAAGTTTACTCATATAT 1246
QY 4854 ACTTTAGATGATTTAAACTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 4913
Db 1245 ACTTTAGATGATTTAAACTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 1186
QY 4914 TGATAATCTCATGACCAAAATCCCTTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4973

Db 1185 TGATAATCTCATGACCAAAATCCCTTAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1126
QY 4974 CGTAGAAAAGATCAAAAGATCTTCTGAGATCCTTTTCTGCGCGTAATCTGCTGCTT 5033
Db 1125 CGTAGAAAAGATCAAAAGATCTTCTGAGATCCTTTTCTGCGCGTAATCTGCTGCTT 1066
QY 5034 GCRAACAAAAAACCCAGCTTACAGCGGTGCTTGTGTCGGATCAAGAGCTACCAAC 5093
Db 1065 GCRAACAAAAAACCCAGCTTACAGCGGTGCTTGTGTCGGATCAAGAGCTACCAAC 1006
QY 5094 TCTTTTCCGAAGTAACTGGCTTACAGAGCGCAGATACCAATATCTGTCTTCTTCTAGT 5153
Db 1005 TCTTTTCCGAAGTAACTGGCTTACAGAGCGCAGATACCAATATCTGTCTTCTTCTAGT 946
QY 5154 GTAGCGGTAGTGGCCACCACCTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCT 5213
Db 945 GTAGCGGTAGTGGCCACCACCTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCT 886
QY 5214 GCTAATCTGTACAGTGGCTGCTGCGAGTAAAGTGGCTGCTTACCGGTTTGGGA 5273
Db 885 GCTAATCTGTACAGTGGCTGCTGCGAGTAAAGTGGCTGCTTACCGGTTTGGGA 826
QY 5274 CTCAGACGATAGTTACCGGATAGCGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 5333
Db 825 CTCAGACGATAGTTACCGGATAGCGCGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 766
QY 5334 ACAGCCGAGCTTGGAGCGACGCTTACCGAGTAAAGTGGCTGCTGCTGCTGCTGCTGCT 5393
Db 765 ACAGCCGAGCTTGGAGCGACGCTTACCGAGTAAAGTGGCTGCTGCTGCTGCTGCTGCT 706
QY 5394 AGAAGCGCCACCTTCCCGAAGGAGGAGGCGAGTATCCGGTAAAGCGGAGGCT 5453
Db 705 AGAAGCGCCACCTTCCCGAAGGAGGAGGCGAGTATCCGGTAAAGCGGAGGCT 646
QY 5454 CGAAGCAGGAGCGCAAGGAGGCTTCCAGGGGAGGCTTCCAGGGGAGGCTTCTTATAGTCC 5513
Db 645 CGAAGCAGGAGCGCAAGGAGGCTTCCAGGGGAGGCTTCCAGGGGAGGCTTCTTATAGTCC 586
QY 5514 TGTGCGGTTTCCGCACTCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5573
Db 585 TGTGCGGTTTCCGCACTCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
QY 5574 GAGCTTATGAAAAACCGCAGCAACCGGCTTCTTACGGTTCCTGCGCTTCTTCTGCTGCT 5633
Db 525 GAGCTTATGAAAAACCGCAGCAACCGGCTTCTTACGGTTCCTGCGCTTCTTCTGCTGCT 466
QY 5634 TTTTGTCTCATGTTCTTTCTGCTGCTTATCCCTGATTCCTGCTGCTGCTGCTGCTGCTGCT 5693
Db 465 TTTTGTCTCATGTTCTTTCTGCTGCTTATCCCTGATTCCTGCTGCTGCTGCTGCTGCTGCT 406
QY 5694 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5753
Db 405 CTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346
QY 5754 CGAGGAAGCGGAGGCGGCTTACGCAAAACCGCTCTCCCGCGCTGCTGCTGCTGCTGCTGCT 5813
Db 345 CGAGGAAGCGGAGGCGGCTTACGCAAAACCGCTCTCCCGCGCTGCTGCTGCTGCTGCTGCT 286
QY 5814 TTAATGCTAG 5822
Db 285 TTAATGCTAG 277

RESULT 9
AX591141/c
LOCUS
AX591141
DEFINITION
Sequence 6 from Patent WO02085932.
ACCESSION
AX591141
VERSION
AX591141.1
GI:27949651
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
linear PAT 27-JAN-2003

artificial sequences.	
1	
REFERENCE	Sablon,E., van Broekhoven,A., Bosman,A., Depla,E. and Deschamps,G.
AUTHORS	Constructs and methods for expression of recombinant hcv envelope
TITLE	proteins
JOURNAL	Patent: WO 02085932-A 6 31-OCT-2002;
INNOVATION	INOGENETICS N.V. (BE)
FEATURES	Location/Qualifiers
source	1..3448
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="vector pGEMTE16H6"
ORIGIN	
Query Match	46.1%; Score 2683.4; DB 6; Length 3448;
Best Local Similarity	99.4%; Pred. No. 0;
Matches 2693; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
QY	3114 CGCGCGATCGGACGTCGGGCCCAATTCGGCTATAGTGAGTGGTATTAACAATTCACCTGG 3173
DB	2985 CGGAGATCGGACGTCGGGCCCAATTCGGCTATAGTGAGTGGTATTAACAATTCACCTGG 2926
QY	3174 CCGTCGTTTTACAACGTCGTGACTGGGAAACCCCTGGCGTTACCCAACTTAATTCGCTTG 3233
DB	2925 CCGTCGTTTTACAACGTCGTGACTGGGAAACCCCTGGCGTTACCCAACTTAATTCGCTTG 2866
QY	3234 CAGCAATCCGCTTCGCCAGTCGGGTAATAGCGAAGGCGCGCACCGATCGCCCTT 3293
DB	2865 CAGCACATCCGCTTCGCCAGTCGGGTAATAGCGAAGGCGCGCACCGATCGCCCTT 2806
QY	3294 CCCAACAGTTGCGCAGGCTGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGC 3353
DB	2805 CCCAACAGTTGCGCAGGCTGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGC 2746
QY	3354 GGGGGGTGGTGGTTACGGCGAGCGTGAACGGTACACTTGGCGAGCGCCCTAGGCGCCG 3413
DB	2745 GGGGGGTGGTGGTTACGGCGAGCGTGAACGGTACACTTGGCGAGCGCCCTAGGCGCCG 2686
QY	3414 TCCTTCGCTTCCTTCCTTCCTTCGCGACGTCGCGCGCTTCGCCGTCAAGCTCT 3473
DB	2685 TCCTTCGCTTCCTTCCTTCCTTCGCGACGTCGCGCGCTTCGCCGTCAAGCTCT 2626
QY	3474 AAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACTCGACCGCAAAA 3533
DB	2625 AAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACTCGACCGCAAAA 2566
QY	3534 ACTTGATTTGGGTGATGGTTCACGTAGTGGCCATCGCCGTGATAGACGGTTTTTCGCC 3593
DB	2565 ACTTGATTTGGGTGATGGTTCACGTAGTGGCCATCGCCGTGATAGACGGTTTTTCGCC 2506
QY	3594 TTTGACGTTGGAGTCCACGGTTCTTTAATAGTGGACTCTTGTCCAAACTGGAAACAAC 3653
DB	2505 TTTGACGTTGGAGTCCACGGTTCTTTAATAGTGGACTCTTGTCCAAACTGGAAACAAC 2446
QY	3654 CAACCCCTATCTCGGCTATTCTTTGATTTAAGGGAATTTTCGGATTTTCGGCTATTG 3713
DB	2445 CAACCCCTATCTCGGCTATTCTTTGATTTAAGGGAATTTTCGGATTTTCGGCTATTG 2386
QY	3714 GTTAAAAATCGCTGATTTAAACAAATTTAAACGCGAATTTTAAACAAATATTAAAGCTT 3773
DB	2385 GTTAAAAATCGCTGATTTAAACAAATTTAAACGCGAATTTTAAACAAATATTAAAGCTT 2326
QY	3774 TACAATTTTCGGCTGATGGGTATTTTTCCTTTCCTTACGCATCTGTGGGTATTTACACCGCA 3833
DB	2325 TACAATTTTCGGCTGATGGGTATTTTTCCTTTCCTTACGCATCTGTGGGTATTTACACCGCA 2266
QY	3834 TACAGGTGCATTTTCGGGGAATTTGGCGGGAACCCCTATTGTTTATTTCCTAAAT 3893
DB	2265 TACAGGTGCATTTTCGGGGAATTTGGCGGGAACCCCTATTGTTTATTTCCTAAAT 2206
QY	3894 ACAATTCAAATATGTTATCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTG 3953
DB	2205 ACAATTCAAATATGTTATCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTG 2146
QY	3954 AAAAAGGAGAGTATGAGTATTTCAACATTTCCGGTGGCCCTTATTCCTCTTTTGGGC 4013
DB	2145 AAAAAGGAGAGTATGAGTATTTCAACATTTCCGGTGGCCCTTATTCCTCTTTTGGGC 2086
QY	4014 ATTTTGGCTTCCTGTTTTTGTCTCACCCAGAAACGCTGGTGAAGATAAAGATGCTGAAGA 4073
DB	2085 ATTTTGGCTTCCTGTTTTTGTCTCACCCAGAAACGCTGGTGAAGATAAAGATGCTGAAGA 2026
QY	4074 TCAGTTGGGTGACAGAGTGGGTATCATCGAATCGGATCTCAACAGCGGTAGATCCCTTGA 4133
DB	2025 TCAGTTGGGTGACAGAGTGGGTATCATCGAATCGGATCTCAACAGCGGTAGATCCCTTGA 1966
QY	4134 GAGTTTTTCGCCCGGAAAGACGTTTTTCCAAATGATGAGCACTTTTAAAGATTCTGCTATGTGG 4193
DB	1965 GAGTTTTTCGCCCGGAAAGACGTTTTTCCAAATGATGAGCACTTTTAAAGATTCTGCTATGTGA 1906
QY	4194 CGCGGTATTAATCCCGTATTGACCGCGGCAAGACCACTCGGTGCCGCATACACTATTTC 4253
DB	1905 TACACTATTATCCCGTATTGACCGCGGCAAGACCACTCGGTGCCGCAGGTATTC 1846
QY	4254 TCAGAATGACTGGTTGAGTACTCACAGTACAGAAAAAGCATTTACGATGGCATGAC 4313
DB	1845 TCAGAATGACTGGTTGAGTACTCACAGTACAGAAAAAGCATTTACGATGGCATGAC 1786
QY	4314 AGTAAGAGAAATTAATCAGCTGCTGCCATAACCATGATGATAACTGCGGGCAACTTACT 4373
DB	1785 AGTAAGAGAAATTAATCAGCTGCTGCCATAACCATGATGATAACTGCGGGCAACTTACT 1726
QY	4374 TGTGACAGATCGGAGACCGAAGAGCTAACCGCTTTTGTGACACACATGGGGGATCA 4433
DB	1725 TGTGACAGATCGGAGACCGAAGAGCTAACCGCTTTTGTGACACACATGGGGGATCA 1666
QY	4434 TGTAACTCGCTTTGATCGTTGGGAAACCGAGCTGAATGAAGCCATACCAACCGAGCG 4493
DB	1665 TGTAACTCGCTTTGATCGTTGGGAAACCGAGCTGAATGAAGCCATACCAACCGAGCG 1606
QY	4494 TGACACCGATCGCTGTAGCAATGCGCAACAAAGTTGCGCAACTATTAACTGGCGAAT 1546
DB	4554 ACTTACTCTAGCTTCGCGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGAG 4613
QY	1545 ACTTACTCTAGCTTCGCGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGAG 1486
QY	4614 ACCACTTTCGCTCGCGCTTCGCGCTTCGCGCTGGCTTTATTTGCTGATAAATCTGGAGCGG 4673
DB	1485 ACCACTTTCGCTCGCGCTTCGCGCTTCGCGCTGGCTTTATTTGCTGATAAATCTGGAGCGG 1426
QY	4674 TGAGCGTGGGTCTCGCGGTATCATTTGACAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT 4733
DB	1425 TGAGCGTGGGTCTCGCGGTATCATTTGACAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT 1366
QY	4734 CGTAGTTATCTACACGCGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGC 4793
DB	1365 CGTAGTTATCTACACGCGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGC 1306
QY	4794 TGAGATAGGTGCTCTCATTAAGCAATTTGGTAACTGTGACAGCAAGTTTACTCATATAT 4853
DB	1305 TGAGATAGGTGCTCTCATTAAGCAATTTGGTAACTGTGACAGCAAGTTTACTCATATAT 1246
QY	4854 ACTTTAGATTGATTTAAACTTCATTTTAAATTTAAAGACTCTAGGTCAAGATCCTTTT 4913
DB	1245 ACTTTAGATTGATTTAAACTTCATTTTAAATTTAAAGACTCTAGGTCAAGATCCTTTT 1186
QY	4914 TGATAATCTCATGACCAAAATCCCTTTAAGCTGAGTTTTTCCTTCCACTGAGCGTCAAGCCC 4973
DB	1185 TGATAATCTCATGACCAAAATCCCTTTAAGCTGAGTTTTTCCTTCCACTGAGCGTCAAGCCC 1126
QY	4974 CGTAGAAAAGATCAAAAGGATCTCTCTTGAGATCCCTTTTTTTCGCGGCTAATCTGCTGCTT 5033
DB	1125 CGTAGAAAAGATCAAAAGGATCTCTCTTGAGATCCCTTTTTTTCGCGGCTAATCTGCTGCTT 1063

		/note="from Human cytomegalovirus immediate early 1 (IE-1) gene" 437..456		
	misc_feature	/note="multiple cloning site"		
	terminator	457..583		
	CDS	/note="Simian virus 40 derived polyA terminator"		
		1465..2325		
		/functions="ampicillin resistance"		
		/codon_start=1		
		/product="beta lactamase"		
		/protein_id="AA082245.1"		
		/db_xref="GI:22001013"		
		/translation="MSIQHVRVALIIPFFAFCLPVAHPBTLVKVDAEDQLGARVGY IELDLSKILKESFRPERFPMSTTFKVLICHTLLSRIDAGQOLGRARYSONDLIVE YSVTKHLDTGMVRELCSAATMSDNTANALLLTIGGPKELTAFLLHNMGDHVRFL DRWPELNEAIPNDERDTPMPVAMPTTLRLKLTGELITLASRQQLIMWADVAGPL LRSALPAGWFIADKSGAGERSGIIAALGPDGPKSRIVVIYITGSAQTMERNRQIA EIGASLIKHW"		
ORIGIN				
	Query Match	46.1%; Score 2693.4; DB 12; Length 3551;		
	Best Local Similarity	99.4%; Pred. No. 0;		
	Matches 2693; Conservative	0; Mismatches 16; Indels 0; Gaps 0;		
QY	3114	CGGCCGATCGGACGTCGGCCCAATTCGCCCTATAGTGAAGTCAATCAATCTACTGG	3173	
DB	612	CGGGACATCGGACGTCGGGCCCAATTCGCCCTATAGTGAAGTCAATCAATCTACTGG	671	
QY	3174	CGCTCGTTTACAACTGCTGACGTGGGAAACCTCGCGTTACCCAACTTAATCGCCTTG	3233	
DB	672	CGCTCGTTTACAACTGCTGACGTGGGAAACCTCGCGTTACCCAACTTAATCGCCTTG	731	
QY	3234	CAGCAATCCCTTTGCGCAGTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT	3293	
DB	732	CAGCAATCCCTTTGCGCAGTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT	791	
QY	3294	CCCAACAGTTGCGACGCTGAAATGGCGAATGACGCGCCCTGTAGCGGCGCATTAAGCG	3353	
DB	792	CCCAACAGTTGCGACGCTGAAATGGCGAATGACGCGCCCTGTAGCGGCGCATTAAGCG	851	
QY	3354	GGCGGTGTGGTGTACGCGCAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGC	3413	
DB	852	GGCGGTGTGGTGTACGCGCAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGC	911	
QY	3414	TGCTTTGCTTTCTTCCCTTCCCTTCTCGCCAGTTCGCGGCTTTCCTCGCTCAAGCTCT	3473	
DB	912	TGCTTTGCTTTCTTCCCTTCCCTTCTCGCCAGTTCGCGGCTTTCCTCGCTCAAGCTCT	971	
QY	3474	AAATCGGGGCTCCCTTTAGGGTTCGATTTAGAGCTTTACGGACCTCGACGCAAAA	3533	
DB	972	AAATCGGGGCTCCCTTTAGGGTTCGATTTAGAGCTTTACGGACCTCGACGCAAAA	1031	
QY	3534	ACTGATTTGGGTGATGTTACAGTGGGCGCATCGCCCTGATAGACGGTTTTTCGCC	3593	
DB	1032	ACTGATTTGGGTGATGTTACAGTGGGCGCATCGCCCTGATAGACGGTTTTTCGCC	1091	
QY	3594	TTTGAGTTTGGAGTCCAGCTTCTTTAAATAGTGGACTCTTGTTCCTGATAGACGCT	3653	
DB	1092	TTTGAGTTTGGAGTCCAGCTTCTTTAAATAGTGGACTCTTGTTCCTGATAGACGCT	1151	
QY	3654	CAACCTTATCTCGCTCTATCTTTTGGATTTAAGGGATTTTGGGATTTTCGGCTATTG	3713	
DB	1152	CAACCTTATCTCGCTCTATCTTTTGGATTTAAGGGATTTTGGGATTTTCGGCTATTG	1211	
QY	3714	GTTAAAAATAGCTGATTTAAACAAATTTTAAACCGGAATTTTAAACAAATTTAACGTT	3773	
DB	1212	GTTAAAAATAGCTGATTTTAAACAAATTTTAAACCGGAATTTTAAACAAATTTAACGTT	1271	
QY	3774	TACAAATTTGCGCTGATGGGTATTTTTCCTTACGATCTGTCGGGTATTTTCAACCGCA	3833	
DB	1272	TACAAATTTGCGCTGATGGGTATTTTTCCTTACGATCTGTCGGGTATTTTCAACCGCA	1331	
QY	3834	TACAGTGGCACTTTTCGGGGAATGTGCGCGGAACCCCTATTGTGTTATTTTCTAAAT	3893	
DB	1332	TACAGTGGCACTTTTCGGGGAATGTGCGCGGAACCCCTATTGTGTTATTTTCTAAAT	1391	
QY	3894	ACATTTCAATATGATCCGCTCATGAGACAATTAACCTGTATAATGCTTCAATAATATG	3953	
DB	1392	ACATTTCAATATGATCCGCTCATGAGACAATTAACCTGTATAATGCTTCAATAATATG	1451	
QY	3954	AAAAAGGAAGATGATGATTTCAAACTTTCCGTGTCGCCCTTATTCCTTTTTCGGCG	4013	
DB	1452	AAAAAGGAAGATGATGATTTCAAACTTTCCGTGTCGCCCTTATTCCTTTTTCGGCG	1511	
QY	4014	ATTTTGCTTCTCTGTTTTTCTCTCAACAGAAAACGCTGGTGAAGTGAAGATGCTGAAGA	4073	
DB	1512	ATTTTGCTTCTCTGTTTTTCTCTCAACAGAAAACGCTGGTGAAGTGAAGATGCTGAAGA	1571	
QY	4074	TCAGTTGGGTGACGAGTGGGTTTACATCGAATGGAATCTCAACAGCGGTGAAGTCTTGA	4133	
DB	1572	TCAGTTGGGTGACGAGTGGGTTTACATCGAATGGAATCTCAACAGCGGTGAAGTCTTGA	1631	
QY	4134	GAGTTTTTCGCCCGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGCG	4193	
DB	1632	GAGTTTTTCGCCCGAAGAACGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGCA	1691	
QY	4194	CGCGGTATTATCCGTTATTGAACCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTC	4253	
DB	1692	TACACTATTATCCGTTATTGAACCGCGGCAAGAGCAACTCGGTGCGCGCGGTATTC	1751	
QY	4254	TCAGATGACTTTGGTTGAGTACTCACAGTCAAGAAAAGCATCTTACGGATGGCATGAC	4313	
DB	1752	TCAGATGACTTTGGTTGAGTACTCACAGTCAAGAAAAGCATCTTACGGATGGCATGAC	1811	
QY	4314	AGTAAGAGAAATTATGACGTGCTGCCATAACCATGAGTGATTAACACGTCGCGCAACTTACT	4373	
DB	1812	AGTAAGAGAAATTATGACGTGCTGCCATAACCATGAGTGATTAACACGTCGCGCAACTTACT	1871	
QY	4374	TTTGCAACAGATCGGAGGACCGAAGAGCTAAACCGCTTTTTTGCACAACATGGGGATCA	4433	
DB	1872	TTTGCAACAGATCGGAGGACCGAAGAGCTAAACCGCTTTTTTGCACAACATGGGGATCA	1931	
QY	4434	TGTAATCGCTTGTATCGTTGGGACCGGAGCTGATGAAGCCATACAAAACGACGAG	4493	
DB	1932	TGTAATCGCTTGTATCGTTGGGACCGGAGCTGATGAAGCCATACAAAACGACGAG	1991	
QY	4494	TGACACCAAGATCGCTGTAGCAATGGCAACAACTTGGCCAACTATTAACCTGGCCAACT	4553	
DB	1992	TGACACCAAGATCGCTGTAGCAATGGCAACAACTTGGCCAACTATTAACCTGGCCAACT	2051	
QY	4554	ACTTACTTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGCGGATATAAGTTGACAG	4613	
DB	2052	ACTTACTTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGCGGATATAAGTTGACAG	2111	
QY	4614	ACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCCGG	4673	
DB	2112	ACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCCGG	2171	
QY	4674	TGAGCGTGGGTCTCGCGGTATCATTTGACAGCACTGGGGCCAGATGTAAGCCCTCCCGTAT	4733	
DB	2172	TGAGCGTGGGTCTCGCGGTATCATTTGACAGCACTGGGGCCAGATGTAAGCCCTCCCGTAT	2231	
QY	4734	CGTAGTTATCTACAGCAAGGAGTCAAGGCAACTATGATGAACGAAATAGACAGATCGC	4793	
DB	2232	CGTAGTTATCTACAGCAAGGAGTCAAGGCAACTATGATGAACGAAATAGACAGATCGC	2291	
QY	4794	TGAGATAGTGCCTCACGACGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGT	4853	
DB	2292	TGAGATAGTGCCTCACGACGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAGTGGT	2351	
QY	4854	ACTTTAGATTTGATTTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCTTTT	4913	
DB	2352	ACTTTAGATTTGATTTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCTTTT	2411	
QY	4914	TGATAATCTCATGACCAAAATCCCTTAAAGTGAAGTTTTCCTTCCACTGAGCGTCAAGCCC	4973	

Db 2412 TGATATCTCATGACCAAAATCCCTTAAAGTGGTTCCTCCACTGAGCGTCAGACCC 2471

QY 4974 COTAGAAAAGATCAAAAGGATCTCTTGTAGATCCTTTTCTGCGGTAAATCTGCTGCTT 5033

Db 2472 COTAGAAAAGATCAAAAGGATCTCTTGTAGATCCTTTTCTGCGGTAAATCTGCTGCTT 2531

QY 5034 GCACACAAAACACACCGCTACACGGGTGGTTCCTGCGGATCAAGAGTACCAAC 5093

Db 2532 GCACACAAAACACACCGCTACACGGGTGGTTCCTGCGGATCAAGAGTACCAAC 2591

QY 5094 TCTTTTCCGAAGGTAACTGGCTTCAGCAGCGCGAGATACCAATACTCTCTCTAGT 5153

Db 2592 TCTTTTCCGAAGGTAACTGGCTTCAGCAGCGCGAGATACCAATACTCTCTCTAGT 2651

QY 5154 GTAGCCGTATGTTAGGCGACACCTTCAAGAACTCTGTAGACACCGCTTACATACCTCGCTCT 5213

Db 2652 GTAGCCGTATGTTAGGCGACACCTTCAAGAACTCTGTAGACACCGCTTACATACCTCGCTCT 2711

QY 5214 GCTAATCTGTTTACAGTGGCTGCTGCCAGTGGGATAGTCTGTCTTACCGGTTGGA 5273

Db 2712 GCTAATCTGTTTACAGTGGCTGCTGCCAGTGGGATAGTCTGTCTTACCGGTTGGA 2771

QY 5274 CTCACAGCATAGTTACCGGATAAGCGCGACGCGTCCGGCTGAAACGGGGGGTTCGTGCAC 5333

Db 2772 CTCACAGCATAGTTACCGGATAAGCGCGACGCGTCCGGCTGAAACGGGGGGTTCGTGCAC 2831

QY 5334 ACAGCCAGCTTGGAGGAAACGCTTACACCGAACTGAGATACCTACAGGCTGAGCTATG 5393

Db 2832 ACAGCCAGCTTGGAGGAAACGCTTACACCGAACTGAGATACCTACAGGCTGAGCTATG 2891

QY 5394 AGAAGCGCACGCTTCCGAAGGAGAAAGCGGACAGGTATCCGTAAAGCGCGAGGCT 5453

Db 2892 AGAAGCGCACGCTTCCGAAGGAGAAAGCGGACAGGTATCCGTAAAGCGCGAGGCT 2951

QY 5454 CGAAACAGGAGAGCGACAGGAGGAGCTTCCAGGGGGAAACGCGCTGTATCTTTATAGTCC 5513

Db 2952 CGAAACAGGAGAGCGACAGGAGGAGCTTCCAGGGGGAAACGCGCTGTATCTTTATAGTCC 3011

QY 5514 TGTGGGTTTCGCCACCTCTGACTTGTAGAGCTGATTTTGTGATGCTCTGTCAGGGGGCG 5573

Db 3012 TGTGGGTTTCGCCACCTCTGACTTGTAGAGCTGATTTTGTGATGCTCTGTCAGGGGGCG 3071

QY 5574 GAGCCTATGAAAACCGCAGACCGCGCTTTTACGGTTCCTGGCTTTTGTCTGCTGCC 5633

Db 3072 GAGCCTATGAAAACCGCAGACCGCGCTTTTACGGTTCCTGGCTTTTGTCTGCTGCC 3131

QY 5634 TTTTGTCTCAATGTTCTTCTGCTGCTTATCCCTGATTTCTGTGATTAACCGTATTACCGC 5693

Db 3132 TTTTGTCTCAATGTTCTTCTGCTGCTTATCCCTGATTTCTGTGATTAACCGTATTACCGC 3191

QY 5694 CTTTGTAGTGAAGTATACCGCTCCCGCAGCGCGAAACCGACCGAGCGAGCGAGTCAAGTGA 5753

Db 3192 CTTTGTAGTGAAGTATACCGCTCCCGCAGCGCGAAACCGACCGAGCGAGCGAGTCAAGTGA 3251

QY 5754 CGAGGAGCGGAAAGAGCGCCCAATACGCAACCGCTCTCCCGCGGTTCGCGGATTC 5813

Db 3252 CGAGGAGCGGAAAGAGCGCCCAATACGCAACCGCTCTCCCGCGGTTCGCGGATTC 3311

QY 5814 TTAATGCAG 5822

Db 3312 TTAATGCAG 3320

RESULT 12

LOCUS AF525778

DEFINITION Expression vector pCMH285, complete sequence.

ACCESSION AF525778

VERSION AF525778.1

KEYWORDS GI:22000815

SOURCE Expression vector pCMH285

ORGANISM Expression vector pCMH285

artificial sequences; vectors.

REFERENCE 1 (bases 1 to 3711)

AUTHORS Hardy, C.M.

TITLE Direct Submission

JOURNAL Submitted (30-JUN-2002) Wildlife, Pests and Diseases, CSIRO Sustainable Ecosystems, GPO Box 284, Canberra, ACT 2601, Australia

FEATURES

source

1..3711

/organism="Expression vector pCMH285"

/mol_type="genomic DNA"

/db_xref="taxon:202036"

66..434

/notes="from Human cytomegalovirus immediate early 1 (IE-1) gene"

437..460

/misc_feature

/notes="multiple cloning site"

459..730

/terminator

/notes="from Human cytomegalovirus immediate early 1 (IE-1) gene"

1625..2485

/function="ampicillin resistance"

/codon_start=1

/product="beta lactamase"

/protein_id="AAM8286.1"

/db_xref="GI:22000815"

/translation="MSIQHFRVALIPFFAAFLPFAHPETLVKVKDAEDQLGARVGY IELDLSGKILSFEPERFPMSTMSTNDNTAANLLLTIGGKELTFLHNMGHVPL YSPVTEKHLTDGTVBELCSAATMSDNTAANLLLTIGGKELTFLHNMGHVPL DRWPELNEALPNDERDTPVAMPPTLRLKLLTGELLTLASRQQLIDMEADKVGPL LRSALPAGFIADKSGAGRGSRGIIAALGPDGPKSRIVVITYITGSAITDERNRQIA EIGASLIKHW"

ORIGIN

Query Match 46.1%; Score 2683.4; DB 12; Length 3711;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2693; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3114 CGCGCGATCGAGCTCGGCGCCCAATTCGCCCTATAGTAGTGTATTAACAATCACTGG 3173

Db 772 CGGAGCATCGGAGCTCGGCGCCCAATTCGCCCTATAGTAGTGTATTAACAATCACTGG 831

QY 3174 CGTCGCTTTTACAACTGCGTGAATGGGAAAACCCCTGGCGTTACCCAACTTAATCGCCTTG 3233

Db 832 CGTCGCTTTTACAACTGCGTGAATGGGAAAACCCCTGGCGTTACCCAACTTAATCGCCTTG 891

QY 3234 CAGCATATCCCTTTTCGCGAGCTGGCGTAATAGCAGAGGGCCGCGACCGATCGCCTT 3293

Db 892 CAGCATATCCCTTTTCGCGAGCTGGCGTAATAGCAGAGGGCCGCGACCGATCGCCTT 951

QY 3294 CCACACAGTTTCGCGAGCTGAATGGCGAATGGAGCGCCCTGTAGCGCGCATTAAGCGC 3353

Db 952 CCACACAGTTTCGCGAGCTGAATGGCGAATGGAGCGCCCTGTAGCGCGCATTAAGCGC 1011

QY 3354 GCGCGGTGTGTGTGTGTAGCGCGAGCTGACCGCTACACTTGTGCGAGCGCCCTAGCGCGCCG 3413

Db 1012 GCGCGGTGTGTGTGTGTAGCGCGAGCTGACCGCTACACTTGTGCGAGCGCCCTAGCGCGCCG 1071

QY 3414 TCCTTTTCGCTTTCTTCTCCCTTCTTCTCGCACCTTCGCGGCTTTCGCCGCTCAAGCTCT 3473

Db 1072 TCCTTTTCGCTTTCTTCTCCCTTCTTCTCGCACCTTCGCGGCTTTCGCCGCTCAAGCTCT 1131

QY 3474 AATCGGGGGCTCCCTTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTTCGACCGCAAAA 3533

Db 1132 AATCGGGGGCTCCCTTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTTCGACCGCAAAA 1191

QY 3534 ACTTGATTTGGGTGATGTTTACGTAGTGGGCCATCGCCCTGTAGACGGTTTTTCGCC 3593

Db 1192 ACTTGATTTGGGTGATGTTTACGTAGTGGGCCATCGCCCTGTAGACGGTTTTTCGCC 1251

QY 3594 TTTGACGTTGGAGTCCACGTTCTTTTATAGTGGACTCTTGTCCAAACTGGAACAACACT 3653

Db 1252 TTTGACGTTGGAGTCCACGTTCTTTTATAGTGGACTCTTGTCCAAACTGGAACAACACT 1311

QY 3654 CAACCTATCTCGCTATTCTTTTGTATTTATAAGGGATTTTTCGCGATTTTCGGCTATTG 3713


```

RESULT 13
CVGEM7LICF/c
LOCUS      3033 bp      DNA      circular SYN 16-MAY-1995
DEFINITION
  Ligation-independent cloning vector pGEM-7zf(+)/LIC-F, complete
  sequence.
ACCESSION
  U25272
VERSION    1
KEYWORDS   beta-lactamase; ligation-independent cloning region; Nari
           restriction site.
SOURCE     Cloning vector pGEM-7zf(+)/LIC-F
           Cloning vector pGEM-7zf(+)/LIC-F
           artificial sequences; vectors.
ORGANISM   1 (bases 1 to 3033)
           Haun,R.S., Serventi,I.M. and Moss,J.
REFERENCE  1 (bases 1 to 3033)
           Rapid, reliable ligation-independent cloning of PCR products using
           modified plasmid vectors
JOURNAL    BioTechniques 13 (4), 515-518 (1992)
MEDLINE    93119606
PUBMED     1362067
REFERENCE  2 (bases 1 to 3033)
           Haun,R.S.
AUTHORS    Direct Submission
TITLE      Submitted (19-APR-1995) Randy S. Haun, NIH, NHLBI, Laboratory of
           Cellular Metabolism, Bldg. 10, Room 5N307, Bethesda, MD 20892-1434,
           USA
COMMENT    Ligation-independent cloning vector. Preparation of the vector for
           cloning includes linearization with Nari, gel purification of the
           linearized vector, and treatment with T4 DNA polymerase in the
           presence of dATP. The target sequence can be amplified using
           sequence specific primers modified at the 5' end to contain an
           additional 13 nucleotides complementary to the vector. The forward
           primer should contain 5'-CTGCTCCGGCA-3', followed by 12-15
           nucleotide target-specific sequence. The reverse primer should
           contain 5'-CTGCTCCGGCA-3', followed by 12-15 nucleotide
           target-specific sequence. The amplified sequence should be gel
           purified and treated with T4 DNA polymerase in the presence of
           dTTP. Annealing of the vector and the amplification product forms a
           duplex that can be used directly for transformation. Sequences
           amplified using these primers are also compatible with the
           pBluescript II KS(+)/LIC vector (ATCC 87047) and pGEM-7zf(+)/LIC-R
           vector (ATCC 87049). Differs from pGEM-7zf(+)/LIC-R (ATCC 87049)
           only in the orientation of complementary ends generated at the
           cloning site. This vector has been deposited in the ATCC repository
           (ATCC 87048).
FEATURES             Location/Qualifiers
     source           1..3033
                     /organism="Cloning vector pGEM-7zf(+)/LIC-F"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39799"
     promoter         /note="pGEM-7zf(+)/LIC-F; ATCC 87048"
                     join(3017..3033,1..6)
                     /note="bacteriophage T7 promoter"
     misc_feature     55..81
                     /product="ligation-independent cloning region"
                     /evidence=experimental
     misc_feature     66..71
                     /product="Nari restriction site"
                     /evidence=experimental
     promoter         complement(151..173)
                     /note="bacteriophage SP6 promoter"
     gene             /gene="lacZ"
                     complement(193..195)
     CDS              /gene="lacZ"
                     /note="initiation codon"
                     /codon_start=1
                     /transl_table=1
                     /protein_id="AAA66386.1"
                     /db_xref="GI:806890"
                     /translation="W"
                     complement(1352..2212)

```

```

/codon_start=1
/transl_table=1
/product="beta-lactamase"
/protein_id="AAA66387.1"
/db_xref="GI:806891"
/translation="MSIQHFRVALIPFFAAFLVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILSRFRPEERFPMWSTFKVLLCGAVLSRIIDAGQQLGRIRHYSQNDLVE
YSPVTEKHLTDGWTVEELCSAATITMSDNTAANLLLTITGGKELTAFLHMGDHVTRL
DRWPELNEAIPIVNDERDTPVAMATILRLKLLGELLTLASROOLLDMWEADKVGPL
LRGSLPAGWFIADKSGAGERGRIIAGLPGDKSRIRIVVITYTGSQATDMDNRRLQA
ETGASLIKHW"
complement(2398..2853)
/standard_name="f1 origin"

ORIGIN
Query Match      46.0%; Score 2677; DB 12; Length 3033;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3146  TATAGTGAGTCGTATTACAAATTCACCTGGCGCGTCTGTTTACAAAGTCGTGACTGGGAAAC 3205
DB      3033  TATAGTGAGTCGTATTACAAATTCACCTGGCGCGTCTGTTTACAAAGTCGTGACTGGGAAAC 2974
QY      3206  CCTGGCGTTTACCAACTTAATCGCTTTCAGACACATCCCCCTTTCGCCAGCTGGCGTAAT 3265
DB      2973  CCTGGCGTTTACCAACTTAATCGCTTTCAGACACATCCCCCTTTCGCCAGCTGGCGTAAT 2914
QY      3266  AGCGAAGAGCCCGACCGATTCGCCCTTCCCAACAGTTGGCGAGCCTGAATGGCGAATGG 3325
DB      2913  AGCGAAGAGCCCGACCGATTCGCCCTTCCCAACAGTTGGCGAGCCTGAATGGCGAATGG 2854
QY      3326  ACCGCCCTCTAGCGGCGCAATTAAGCGCGCGGTGTGTGTTTACCGCGAGCGTGAACCG 3385
DB      2853  ACCGCCCTCTAGCGGCGCAATTAAGCGCGCGGTGTGTGTTTACCGCGAGCGTGAACCG 2794
QY      3386  CTACACTTGCAGCGCCCTAGCGCCGCTCTTTCGCTTTCCTTCCTTCCTTCCTTCGCGCA 3445
DB      2793  CTACACTTGCAGCGCCCTAGCGCCGCTCTTTCGCTTTCCTTCCTTCCTTCCTTCGCGCA 2734
QY      3446  CGTTTCGCGCGCTTTCGCCGCTCAAGCTCTAAATCGGGGCGTCCCTTTAGGGTTCGGAATTA 3505
DB      2733  CGTTTCGCGCGCTTTCGCCGCTCAAGCTCTAAATCGGGGCGTCCCTTTAGGGTTCGGAATTA 2674
QY      3506  GAGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTGGGTGATGTTTACGTAGTGGGC 3565
DB      2673  GAGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTGGGTGATGTTTACGTAGTGGGC 2614
QY      3566  CATCGCCCTGATAGACGGTTCCTTCGCCCTTTCGAGTTGGAGTCCACGTTCTTTAATAGTG 3625
DB      2613  CATCGCCCTGATAGACGGTTCCTTCGCCCTTTCGAGTTGGAGTCCACGTTCTTTAATAGTG 2554
QY      3626  GACTCTTTGTTCCAAACTGGAAACACACTCAACCCCTATCTCGGTCTATCTTTGATTTAT 3685
DB      2553  GACTCTTTGTTCCAAACTGGAAACACACTCAACCCCTATCTCGGTCTATCTTTGATTTAT 2494
QY      3686  AAGGGATTTGCGGATTTTCGSCCTATTGTTTAAAAAATGAGCTGATTTAAACAATATTTA 3745
DB      2493  AAGGGATTTGCGGATTTTCGSCCTATTGTTTAAAAAATGAGCTGATTTAAACAATATTTA 2434
QY      3746  ACGCGAATTTTAAACAAATATTTAACGTTTACAAATTCGCCCTGATGCGGTATTTTCTCCT 3805
DB      2433  ACGCGAATTTTAAACAAATATTTAACGTTTACAAATTCGCCCTGATGCGGTATTTTCTCCT 2374
QY      3806  ACGCATCTGTGGGTATTTCACCGCATACAGTGGCACTTTTCGGGGAAATGTGGCG 3865
DB      2373  ACGCATCTGTGGGTATTTCACCGCATACAGTGGCACTTTTCGGGGAAATGTGGCG 2314
QY      3866  GAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATCCCGTCAATGAGACAAAT 3925
DB      2313  GAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATCCCGTCAATGAGACAAAT 2254
QY      3926  AACCCCTGATTAATGCTTCAATAATATTGAAAAAGAGAGATGATGATTTCAACATTTC 3985

```

Db 2253 AACCCGTGAATAATGCTTCAATAAATATGAAAAAGGAGATGATGAGTAATCAACATTTCC 2194
QY 3986 GTGTCGCCCTTATTCCTCTTTTGGGCAATTTTGCCTTCTGCTTTTGGCTCAACCCAGAAA 4045
Db 2193 GTGTCGCCCTTATTCCTCTTTTGGGCAATTTTGCCTTCTGCTTTTGGCTCAACCCAGAAA 2134
QY 4046 CGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTATACATCGAAC 4105
Db 2133 CGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTATACATCGAAC 2074
QY 4106 TGGATCTCAACAGCGGTAGATCTTGAGAGTTTTGCCCCGGAAGAACGTTTTCCAAATGA 4165
Db 2073 TGGATCTCAACAGCGGTAGATCTTGAGAGTTTTGCCCCGGAAGAACGTTTTCCAAATGA 2014
QY 4166 TGAGCACTTTTAAAGTTCTGTAATGTGGCGCGTATTTATCCCGTATTGAACGCGGCAAG 4225
Db 2013 TGAGCACTTTTAAAGTTCTGTAATGTGGCGCGTATTTATCCCGTATTGAACGCGGCAAG 1954
QY 4226 AGCAACTCGGTCCGCGATACATATTTCTCAGAAATGACTTTGGTTGAGTACTCCACAGTCA 4285
Db 1953 AGCAACTCGGTCCGCGATACATATTTCTCAGAAATGACTTTGGTTGAGTACTCCACAGTCA 1894
QY 4286 CAGAAAGCATCTTACGATGGCATGACATGAGAGAAATATGAGTGTGCTGCCATACCA 4345
Db 1893 CAGAAAGCATCTTACGATGGCATGACATGAGAGAAATATGAGTGTGCTGCCATACCA 1834
QY 4346 TGAGTGAATACACTGCGGCCAACTTACTTCTGCAACGATCGGAGGACCGAAGAGCTAA 4405
Db 1833 TGAGTGAATACACTGCGGCCAACTTACTTCTGCAACGATCGGAGGACCGAAGAGCTAA 1774
QY 4406 CGCTTTTGTGCAACATGCGGATCATGTAACTCGCTTGATTCGTTGGAAACCGGAGC 4465
Db 1773 CGCTTTTGTGCAACATGCGGATCATGTAACTCGCTTGATTCGTTGGAAACCGGAGC 1714
QY 4466 TGAATGAAGCCATACCAACGACGCGGTGACACACGATGCTGTAGCAATGGCAACAA 4525
Db 1713 TGAATGAAGCCATACCAACGACGCGGTGACACACGATGCTGTAGCAATGGCAACAA 1654
QY 4526 CGTTGCGCAACTTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAG 4585
Db 1653 CGTTGCGCAACTTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAG 1594
QY 4586 ACTGGATGAGGCGGATTAAGTTGAGAACCACTTCTGCGCTGCGCCCTTCGCGTGGCT 4645
Db 1593 ACTGGATGAGGCGGATTAAGTTGAGAACCACTTCTGCGCTGCGCCCTTCGCGTGGCT 1534
QY 4646 GGTTTATTCTGATAAATCTGGAGCGGTGAGCGTGGTCTCGCGTATCATTTGACGAC 4705
Db 1533 GGTTTATTCTGATAAATCTGGAGCGGTGAGCGTGGTCTCGCGTATCATTTGACGAC 1474
QY 4706 TGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTATACAGCGGGGAGTCAGGCAA 4765
Db 1473 TGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTATACAGCGGGGAGTCAGGCAA 1414
QY 4766 CTATCGATCAACGAATAGACAGATCGCTGAGATAGTGCCTCACTGATTAAGCATTTGT 4825
Db 1413 CTATCGATCAACGAATAGACAGATCGCTGAGATAGTGCCTCACTGATTAAGCATTTGT 1354
QY 4826 AACTGTGACACCAAGTTTACTCATATATATCTTTAGATTGATTTAAACTTTCAATTTTAA 4885
Db 1353 AACTGTGACACCAAGTTTACTCATATATATCTTTAGATTGATTTAAACTTTCAATTTTAA 1294
QY 4886 TTAAGAGATCTAGTGAAGATCTTTTGTATTAATCTCATGACCAAAAATCCCTTAACTG 4945
Db 1293 TTAAGAGATCTAGTGAAGATCTTTTGTATTAATCTCATGACCAAAAATCCCTTAACTG 1234
QY 4946 AGTTTTCTGCTCAGCGTCAAGCCCGTGAAGAGATCAAGAGATCTTTTGATC 5005
Db 1233 AGTTTTCTGCTCAGCGTCAAGCCCGTGAAGAGATCAAGAGATCTTTTGATC 1174
QY 5006 CTTTTTTCTGCGGTAAATCTGCTGTGCAACAAAAAACCACCGCTTACCAGCGGTGG 5065
Db 1173 CTTTTTTCTGCGGTAAATCTGCTGTGCAACAAAAAACCACCGCTTACCAGCGGTGG 1114

QY 5066 TTTGTTTGGCGGATCAAGAGCTACCAACTCTTTTTCGAAAGTAACTGGCTTCAGCAGAG 5125
Db 1113 TTTGTTTGGCGGATCAAGAGCTACCAACTCTTTTTCGAAAGTAACTGGCTTCAGCAGAG 1054
QY 5126 CGCAGATACCAATACTGCTCTTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACT 5185
Db 1053 CGCAGATACCAATACTGCTCTTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACT 994
QY 5186 CTGTAGCACCGCTCATATACCTCGCTCTGCTAATCTGTATTACAGTGGCTGTGCCAGTG 5245
Db 993 CTGTAGCACCGCTCATATACCTCGCTCTGCTAATCTGTATTACAGTGGCTGTGCCAGTG 934
QY 5246 GCGATAAGTCTGCTCTTTACCGGTTGCACTCAAGACGATAGTTACCGGATAAGCGCAGC 5305
Db 933 GCGATAAGTCTGCTCTTTACCGGTTGCACTCAAGACGATAGTTACCGGATAAGCGCAGC 874
QY 5306 GGTGCGGCTGAACCGGGGGTTTGTGCACACAGCCAGCTTTGGAGCGAACACCTACACCG 5365
Db 873 GGTGCGGCTGAACCGGGGGTTTGTGCACACAGCCAGCTTTGGAGCGAACACCTACACCG 814
QY 5366 AACTGAGATACCTACAGCGTACCTATGAGAAAGCCGCTTCCGAAAGGAGAAAG 5425
Db 813 AACTGAGATACCTACAGCGTACCTATGAGAAAGCCGCTTCCGAAAGGAGAAAG 754
QY 5426 CGGACAGGTATCCGGTAAAGCGGCGGTGCGAACAGAGAGCGCACAGGAGCTTCCAG 5485
Db 753 CGGACAGGTATCCGGTAAAGCGGCGGTGCGAACAGAGAGCGCACAGGAGCTTCCAG 694
QY 5486 GGGGAAACCGCTGTTATCTTTATGATCTGTGGGTTTCGCCACCTCTGACTTGAAGCTC 5545
Db 693 GGGGAAACCGCTGTTATCTTTATGATCTGTGGGTTTCGCCACCTCTGACTTGAAGCTC 634
QY 5546 GATTTTGTGATCTGCTCAGGGGGCGGAGCTATGAAACCGCAGACCGCGGCT 5605
Db 633 GATTTTGTGATCTGCTCAGGGGGCGGAGCTATGAAACCGCAGACCGCGGCT 574
QY 5606 TTTTACGGTCTCTGGCTTTTGTGGCTTTTGTCTCACATGTTCTTCTGCGTTATCCC 5665
Db 573 TTTTACGGTCTCTGGCTTTTGTGGCTTTTGTCTCACATGTTCTTCTGCGTTATCCC 514
QY 5666 CTGATTTCTGTGATTAACCGTATTACGCTTTTGTAGTGTATACCGCTGCGCGAGCC 5725
Db 513 CTGATTTCTGTGATTAACCGTATTACGCTTTTGTAGTGTATACCGCTGCGCGAGCC 454
QY 5726 GAACACCGAGCGCAGCGAGTCAGTGAGCGAGGAGCGGAGCGCCCAATACGCAAC 5785
Db 453 GAACACCGAGCGCAGCGAGTCAGTGAGCGGAGCGGAGCGCCCAATACGCAAC 394
QY 5786 CGCCTCTCCCCCGGCTTTGGCGGATTCAATTAATGCAG 5822
Db 393 CGCCTCTCCCCCGGCTTTGGCGGATTCAATTAATGCAG 357

RESULT 14
CVGEM7LICR/c
LOCUS 3033 bp DNA circular SYN 16-MAY-1995
DEFINITION Ligation-independent cloning vector pGEM-7zf(+)/LIC-R, complete sequence.
ACCESSION U25268
VERSION 1
KEYWORDS beta-lactamase; ligation-independent cloning region; NarI
SOURCE Cloning vector pGEM-7zf(+)/LIC-R
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 3033)
AUTHORS Haun, R.S., Serventi, I.M. and Moss, J.
TITLE Rapid, reliable ligation-independent cloning of PCR products using modified plasmid vectors
JOURNAL BioTechniques 13 (4), 515-518 (1992)
MEDLINE 93119606
PUBMED 1362067


```
QY 4286 CAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTATGACGTGCTGCCATACCA 4345
| | | | |
Db 1893 CAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTATGACGTGCTGCCATACCA 1834
| | | | |
QY 4346 TGAGTGATACACTCGGGCCAACTTACTTCTGACAGCATCGGAGGACCGAAGAGCTAA 4405
| | | | |
Db 1833 TGAGTGATACACTCGGGCCAACTTACTTCTGACAGCATCGGAGGACCGAAGAGCTAA 1774
| | | | |
QY 4406 CCGCTTTTGTGACAAATCGGGGATCATGTAATCGCTTGTGTTGGAAACCGGAGC 4465
| | | | |
Db 1773 CCGCTTTTGTGACAAATCGGGGATCATGTAATCGCTTGTGTTGGAAACCGGAGC 1714
| | | | |
QY 4466 TGAATGAAGCCATACCAAAACGAGCGGTGACACCCAGCATGCGCTGTAGCAATGGCAACAA 4525
| | | | |
Db 1713 TGAATGAAGCCATACCAAAACGAGCGGTGACACCCAGCATGCGCTGTAGCAATGGCAACAA 1654
| | | | |
QY 4526 CGTTGGCAAACTTAACTTGGGAACTACTTACTTCTAGCTTCCGGCAACAATTAATAG 4585
| | | | |
Db 1653 CGTTGGCAAACTTAACTTGGGAACTACTTACTTCTAGCTTCCGGCAACAATTAATAG 1594
| | | | |
QY 4586 ACTGGATGGAGCGGATAAAGTTGACGAGCACCTTCTGCGCTCGGCCCTTCCGGCTGGCT 4645
| | | | |
Db 1593 ACTGGATGGAGCGGATAAAGTTGACGAGCACCTTCTGCGCTCGGCCCTTCCGGCTGGCT 1534
| | | | |
QY 4646 GGTTTATTGCTGATAAATCTGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCAC 4705
| | | | |
Db 1533 GGTTTATTGCTGATAAATCTGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCAC 1474
| | | | |
QY 4706 TGGGGCCAGATGTAAGCCCTCCGGTATCGTAGTTATCTACAGACGGGAGTCAAGCAA 4765
| | | | |
Db 1473 TGGGGCCAGATGTAAGCCCTCCGGTATCGTAGTTATCTACAGACGGGAGTCAAGCAA 1414
| | | | |
QY 4766 CTATGGATGAACGAAATPAGACAGATCGCTGAGATAGTGTGCTCACTGATTAAAGCATTTGGT 4825
| | | | |
Db 1413 CTATGGATGAACGAAATPAGACAGATCGCTGAGATAGTGTGCTCACTGATTAAAGCATTTGGT 1354
| | | | |
QY 4826 AACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTGATTTTAAACTTCATTTTAAAT 4885
| | | | |
Db 1353 AACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTGATTTTAAACTTCATTTTAAAT 1294
| | | | |
QY 4886 TTAATAAGGATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAAGTG 4945
| | | | |
Db 1293 TTAATAAGGATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAAGTG 1234
| | | | |
QY 4946 AGTTTTCGTTCCTACTGAGCGTCAAGCCCGGTAGAAAAGATCAAGGATCTTCTTGAGATC 5005
| | | | |
Db 1233 AGTTTTCGTTCCTACTGAGCGTCAAGCCCGGTAGAAAAGATCAAGGATCTTCTTGAGATC 1174
| | | | |
QY 5006 CTTTTCCTGCGCGTAATCTGCTGTGCTTGCAAAACAAAACCAACCGCTACCGCGGTGG 5065
| | | | |
Db 1173 CTTTTCCTGCGCGTAATCTGCTGTGCTTGCAAAACAAAACCAACCGCTACCGCGGTGG 1114
| | | | |
QY 5066 TTTTGTTCGGGATCAAGAGTCAACACTCTTTTTCGAGGTAACCTGGCTTCCAGCAGAG 5125
| | | | |
Db 1113 TTTTGTTCGGGATCAAGAGTCAACACTCTTTTTCGAGGTAACCTGGCTTCCAGCAGAG 1054
| | | | |
QY 5126 CGCAGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTTAGCCACCACTTCAAGAACT 5185
| | | | |
Db 1053 CGCAGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTTAGCCACCACTTCAAGAACT 994
| | | | |
QY 5186 CTTAGACCGCTTACATACCTCGCTCTGCTAATCTGTATCCAGTGGCTGTGCCAGTG 5245
| | | | |
Db 993 CTTAGACCGCTTACATACCTCGCTCTGCTAATCTGTATCCAGTGGCTGTGCCAGTG 934
| | | | |
QY 5246 GCCATAGTCTGCTTACCGGTTGGACTCAGACGATAGTTTACCGGTAAGGCCGAGC 5305
| | | | |
Db 933 GCCATAGTCTGCTTACCGGTTGGACTCAGACGATAGTTTACCGGTAAGGCCGAGC 874
| | | | |
QY 5306 GGTTCGGGCTGAACGGGGGGTTCGTGACACAGCCCGAGCTTGGAGCGAAACGACCTACACCG 5365
| | | | |
Db 873 GGTTCGGGCTGAACGGGGGGTTCGTGACACAGCCCGAGCTTGGAGCGAAACGACCTACACCG 814
| | | | |

RESULT 15
AF041426/c
LOCUS Cloning vector pVLH-1, 7823 bp DNA circular SYN 07-MAR-2000
DEFINITION Cloning vector pVLH-1, complete sequence.
ACCESSION AF041426
VERSION AF041426.1 GI:3025714
KEYWORDS Cloning vector pVLH-1
SOURCE Cloning vector pVLH-1
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 7823)
AUTHORS Deitsch,K.W. and Wellemis,T.E.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1998) LPD/NIAID, NIH, Bldg 4, Rm B1-34, Bethesda, MD 20892, USA
FEATURES
source
1..7823
/organism="Cloning vector pVLH-1"
/mol_type="genomic DNA"
/specific_host="Plasmodium falciparum"
/db_xref="taxon:74888"
/focus
52..2651
/organism="Plasmodium falciparum"
/mol_type="genomic DNA"
/strain="Dd2"
/db_xref="taxon:5833"
/chromosomes="12"
52..2651
/gene="var7b"
52..2651
/gene="var7b"
/promoter
5253..4311
/note="variant surface antigen regulatory region"
CDS
2853..4311
/codon_start=1
/product="luciferase"
/protein_id="AAC12726.1"
/db_xref="GI:3025715"
/translation="MLHEDAKNIKKGPFFPLEDGTAGEQLHKMKRYALVPGTIAF"
```


<p> TDAHIEVDITYAEVEMSVRLAEAMKRYGLNTHRIIVVCSNSLOFPMPVLGALFIGV AVAPNDIYNERLLNSMGIISOPTVVFVSVKGLKOLINVOKKLPIIOKILIMSKTDY QGFOSMTFVISHLPPGNEFYDFPESFDRDKDTIALIMNSGSGTGLPKGVALPHRTAC VRSHARDPIFGNQIIFDTAILSVFPFHGFMETTLIGYLICGFVWVLMYRFEHELPL RSLQDYKIQSALIVPTLISFPAKSTLIDKYLDSLNLHIEIAGGAPLSKEVEGEAVAKRPH LPIRGQYGGTETTSAILITPEGDDKPGAVKVVFPFEAKVVDLDITGKTLGVNORGL CVRGPIMSGVYNNPEATNALIDKDLHSGDIAYWDEDBHFFTVDRLSKLSIKYKGVQ VAPAEISILLOHPNIIPDAGVAGLPDDAGELPAVVVLPHGKTMTEKEIYDVYASQV TTAKLGGVVVDEVEPKGLTGKLDARKIREILIKAKKGGKIAV" complement(6142..7002) /note="ampicillin resistance" /codon_start=1 /product="B-lactamase" /protein_id="AAC12727.1" /db_xref="GI:3025716" /translation="MSIQHFRVALIPFEAFCLPVFAHPETLVKVKDAEDQLGARVGY IEDLNLSGKLESPFERPEPMSTFKVLICGAVLSRIDAGQEQLGRIRHYSQNDLVE YSPVTEKHLDTGMTRPRLCAAMITMSDNTAANLLITIGGPKELTAFIHNMGDHTVPL DRWPELNEAIPNDERDTMPVAMATTLRLKLLTGELLTLASROOLIDWMEADKVGPL LRSALPAGWFIADKSGAGERSGI IAAIGPDGPKPSRIIVLYITGSAQTDWERNRQIA EIGASLIKHV" </p>									
<p> Query Match 46.0%; Score 2677; DB 12; Length 7823; Best Local Similarity 100.0%; Pred. No. 0; Matches 2677; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </p>									
QY	3146	TATAGTGAGTGTATTCAATTCATCTGCGCGTGTGTTTACAACTGCTGAGTACGGAAAC	3205						
Db	7823	TATAGTGAGTGTATTCAATTCATCTGCGCGTGTGTTTACAACTGCTGAGTACGGAAAC	7764						
QY	3206	CCTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAAT	3265						
Db	7763	CCTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCTTTCCGCCAGCTGGCGTAAT	7704						
QY	3266	AGCGAAGAGGCGCCACCGATCGCCCTTCCCAAACAGTTTGGCGACCTGGAATGGCGAATGG	3325						
Db	7703	AGCGAAGAGGCGCCACCGATCGCCCTTCCCAAACAGTTTGGCGACCTGGAATGGCGAATGG	7644						
QY	3326	ACGGCCCTGTAGCGGCGAATAAGCGGCGGGTGTGGTGTACGCGAGCGTGACCG	3385						
Db	7643	ACGGCCCTGTAGCGGCGAATAAGCGGCGGGTGTGGTGTACGCGAGCGTGACCG	7584						
QY	3386	CTACACTTGCAGCGCCCTAGCGCCGCTCTCTTCGTTCTTCCTTCCTTCCTTCGCCA	3445						
Db	7583	CTACACTTGCAGCGCCCTAGCGCCGCTCTCTTCGTTCTTCCTTCCTTCCTTCGCCA	7524						
QY	3446	CGTTGCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCGTCCCTTTAGGGTTCCGATTTA	3505						
Db	7523	CGTTGCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCGTCCCTTTAGGGTTCCGATTTA	7464						
QY	3506	GAGCTTTACGGCACCTCGACGGCAAAACTTGATTTGGGTGATGTTTACGTAGTGGG	3565						
Db	7463	GAGCTTTACGGCACCTCGACGGCAAAACTTGATTTGGGTGATGTTTACGTAGTGGG	7404						
QY	3566	CATCGCCCTGATAGACGTTTTCGCCCTTTGCGCTTTCGAGTGGAGTCCACGCTCTTAAATAGT	3625						
Db	7403	CATCGCCCTGATAGACGTTTTCGCCCTTTGCGCTTTCGAGTGGAGTCCACGCTCTTAAATAGT	7344						
QY	3626	GACTCTTGTTCCAAACCTGGAACACACTCAACCCCTATCTCGGTCTATTCTTTTGTATTAT	3685						
Db	7343	GACTCTTGTTCCAAACCTGGAACACACTCAACCCCTATCTCGGTCTATTCTTTGTATTAT	7284						
QY	3686	AAGGATTTTGGCGATTTCGGCTTATGGTTAAAAATAGAGTGAATTAACAAATATTTA	3745						
Db	7283	AAGGATTTTGGCGATTTCGGCTTATGGTTAAAAATAGAGTGAATTAACAAATATTTA	7224						
QY	3746	ACGGAAATTTTAAACAAATATTACGTTTACAAATTCGCCGTGATGCGGTATTCTCCTT	3805						
Db	7223	ACGGAAATTTTAAACAAATATTACGTTTACAAATTCGCCGTGATGCGGTATTCTCCTT	7164						
QY	3806	ACGCATCTGCGGTATTTCACCGCATACAGTGGCACATTTTCGGGGAAATGTCGCG							

ORIGIN

Db	7163	ACGCATCTGTGCGGTATTTCACACCGCATACAGTGGCACTTTTCGGGGAATGTGCGG	7104						
QY	3866	GAACCCCTATTGTGTTATTTTCTAAATAATTCATTAATATGATTCGCTCATAGACAAAT	3925						
Db	7103	GAACCCCTATTGTGTTATTTTCTAAATAATTCATTAATATGATTCGCTCATAGACAAAT	7044						
QY	3926	AACCTGATATAATGCTTTCAATATATTGAAAAAGGAGAGTATGATATTCAACATTTC	3985						
Db	7043	AACCTGATATAATGCTTTCAATATATTGAAAAAGGAGAGTATGATATTCAACATTTC	6984						
QY	3986	GTGTGCGCCCTATTTCCTTTTCGCGCATTTTCCTTCCTTCCTTTTCCTTCCTTCCTTC	4045						
Db	6983	GTGTGCGCCCTATTTCCTTTTCGCGCATTTTCCTTCCTTCCTTTTCCTTCCTTCCTTC	6924						
QY	4046	CGCTGTGAAGTAAAAAGATGCTGAAGATCAGTTTGGGTGACAGTGGGTTCATATCGAAC	4105						
Db	6923	CGCTGTGAAGTAAAAAGATGCTGAAGATCAGTTTGGGTGACAGTGGGTTCATATCGAAC	6864						
QY	4106	TGGATCTCAACAGCGGTAAAGATCCTTCAGAGTTCCTCGCCCCGGAAGACGTTTTCCTTGA	4165						
Db	6863	TGGATCTCAACAGCGGTAAAGATCCTTCAGAGTTCCTCGCCCCGGAAGACGTTTTCCTTGA	6804						
QY	4166	TGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTATCCGTTATTGACCGCGGCAAG	4225						
Db	6803	TGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTATCCGTTATTGACCGCGGCAAG	6744						
QY	4226	AGCAACTCGGTGCGCGCATACATTTCTCAGAAATGACTTGGTTGAGTACTCAACGATCA	4285						
Db	6743	AGCAACTCGGTGCGCGCATACATTTCTCAGAAATGACTTGGTTGAGTACTCAACGATCA	6684						
QY	4286	CAGAAAAGCATCTTACCGATGGCATGACAGTAAAGAAATATGAGTGTGCTCCATAACCA	4345						
Db	6683	CAGAAAAGCATCTTACCGATGGCATGACAGTAAAGAAATATGAGTGTGCTCCATAACCA	6624						
QY	4346	TGAGTGATAACACTCGCGCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGAGCTAA	4405						
Db	6623	TGAGTGATAACACTCGCGCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGAGCTAA	6564						
QY	4406	CCGCTTTTTCGACAAACATGGGGGATCATGTAACTCGCTTGTATGCTTGGGAAACCGGAGC	4465						
Db	6563	CCGCTTTTTCGACAAACATGGGGGATCATGTAACTCGCTTGTATGCTTGGGAAACCGGAGC	6504						
QY	4466	TGATGAAGCCATACCAAACGAGCGGTGACACACGATGCTGTAGCAATGCGACAA	4525						
Db	6503	TGATGAAGCCATACCAAACGAGCGGTGACACACGATGCTGTAGCAATGCGACAA	6444						
QY	4526	CGTTGCGCAAACTATTAACTGGGAACTACTTACTCTAGCTTCCCGGCAACAAATTAATAG	4585						
Db	6443	CGTTGCGCAAACTATTAACTGGGAACTACTTACTCTAGCTTCCCGGCAACAAATTAATAG	6384						
QY	4586	ACTGGATGGAGGCGGATAAAGTTGACGAGCACTTCTGCGCTCGGCTTCGCGCTGGCT	4645						
Db	6383	ACTGGATGGAGGCGGATAAAGTTGACGAGCACTTCTGCGCTCGGCTTCGCGCTGGCT	6324						
QY	4646	GGTTATTGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCGGTATCATTTGCAGCAC	4705						
Db	6323	GGTTATTGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCGGTATCATTTGCAGCAC	6264						
QY	4706	TGGGGCCAGATGGTAAGCCCTCCGTTATCTAGTTATCTACACGACGGGAGTCAGGCAA	4765						
Db	6263	TGGGGCCAGATGGTAAGCCCTCCGTTATCTAGTTATCTACACGACGGGAGTCAGGCAA	6204						
QY	4766	CTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCAGTGATTAAGCATTTGGT	4825						
Db	6203	CTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCAGTGATTAAGCATTTGGT	6144						
QY	4826	AACGTGACAGCAAGTTTACTCATATATCTTAGATTGATTTTAAAACTCAITTTTAAAT	4885						
Db	6143	AACGTGACAGCAAGTTTACTCATATATCTTAGATTGATTTTAAAACTCAITTTTAAAT	6084						
QY	4886	TTAAAGGATCTAGGTGAAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAAGCTG	4945						
Db	6083	TTAAAGGATCTAGGTGAAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAAGCTG	6024						

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 09:30:17 ; Search time 1367 Seconds

(without alignments)
18092.911 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagacaggtttcccg.....tgccgattcattaatgcag 5822

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_29Jan04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5822	100.0	5822	6 AAS20853	Expressio
2	2757.2	47.4	5534	2 AAT43137	Aat43137 pUMIGIT s
3	2686	46.1	4229	4 AAH25896	Aah25896 Genetic i
4	2683.4	46.1	3448	7 ABQ84197	Abq84197 Vector pG
5	2683.4	46.1	3448	7 AAD50589	Aad50589 pGEMTEISH
6	2680.4	46.0	3448	7 ABT14439	Abt14439 HCV envel
7	2675.4	46.0	3018	2 AAX23905	Aax23905 Plasmid p
8	2675.4	46.0	5919	4 AAD09980	PhSP-GUS
9	2670.2	45.9	3357	7 ACC44700	Acc44700 Plasmid p
10	2670.2	45.9	3357	7 ABT16597	Artificia
11	2668.6	45.8	4514	8 ADA94775	Ada94775 Plasmid p
12	2658.4	45.7	9359	6 ABK11039	Abk11039 pVDH636 v
13	2658.4	45.7	9359	6 ABK10687	Abk10687 Transform
14	2641.4	45.4	3404	8 ADA41728	Ada41728 Plasmid p
15	2634.4	45.2	3968	4 AAD09981	Aad09981 pHSP70-1M
16	2634.4	45.2	4626	4 AAD09988	Aad09988 pHSP-ohox
17	2630.4	45.2	3485	6 AAI72813	Expressio
18	2553	43.9	4965	2 AAV18742	Complete
19	2553	43.9	5109	2 AAV13846	Complete
20	2553	43.9	6196	2 AAV13168	Complete
21	2553	43.9	6243	2 AAV13841	Complete
22	2553	43.9	6503	2 AAV13169	Complete
23	2553	43.9	6959	2 AAV13165	Complete

C 24	2553	43.9	7379	2	AAV13176	Complete
C 25	2553	43.9	8792	2	AAV18745	Complete
C 26	2552	43.8	10078	6	ABQ73047	Tomato an
C 27	2551.8	43.8	37808	2	AAX02780	Vector pM
C 28	2551.4	43.8	8618	2	AAV18741	Complete
C 29	2550	43.8	4883	6	AAD28233	CMV expre
C 30	2550	43.8	7287	2	AAV02042	Plasmid p
C 31	2549.4	43.8	2962	9	ADD14879	Phage dis
C 32	2549.4	43.8	3057	9	ADD14892	Phage dis
C 33	2549.4	43.8	3093	9	ADD14876	Phage dis
C 34	2549	43.8	2958	4	AAS13970	Plasmid p
C 35	2549	43.8	2958	4	AAS13969	Plasmid p
C 36	2549	43.8	2958	4	AAS13971	Plasmid p
C 37	2549	43.8	3351	6	ABT08167	Recombina
C 38	2549	43.8	4754	6	ABT08175	Recombina
C 39	2549	43.8	4773	6	ABT08176	Recombina
C 40	2549	43.8	4831	6	ABT08194	Recombina
C 41	2549	43.8	6345	2	AAX88054	Plasmid p
C 42	2549	43.8	21329	7	AAD48562	Chimeric
C 43	2545.8	43.7	6046	2	AAV13845	Complete
C 44	2545.8	43.7	6245	2	AAV13844	Complete
C 45	2545.8	43.7	6448	2	AAV13843	Complete

ALIGNMENTS

RESULT 1

AAS20853

ID AAS20853 standard; DNA; 5822 BP.

XX

AC AAS20853;

DT 05-JUN-2002 (first entry)

XX Expression cassette, pFP-IRN1 useful for gene silencing.

KW Inhibition of gene expression; expression cassette; inverted repeat; IR;
 KW NOS; nopaline synthase; figwort mosaic virus promoter; FMV; hsp70; PG;
 KW plant heat shock 70; tomato; polygalacturonase; disease resistance;
 KW flavour; nutritional characteristic; plant; gene silencing; pFP-IRN1;
 KW regulating gene expression; mutant; ds.

XX Lycopersicon esculentum.

OS Agrobacterium tumefaciens.

OS Figwort mosaic virus.

OS Synthetic.

OS Chimeric.

XX WO200214472-A2.

XX 21-FEB-2002.

XX 14-AUG-2001; 2001WO-US025538.

XX 15-AUG-2000; 2000US-0225508P.

XX 07-AUG-2001; 2001US-00924197.

XX (DNAP) DNA PLANT TECHNOLOGY CORP.

XX Gutterson N, Oeller P;

XX WPI; 2002-257599/30.

XX Reducing the expression of a target gene in a cell, comprises expressing
 PT in the cell an expression cassette comprising a promoter operably linked
 PT to a sense or antisense targeting sequence and an inverted repeat of a
 PT nopaline synthase gene.

XX Claim 51; Page 37-39; 39pp; English.

XX The present invention relates to an improved method for inhibiting the
 CC expression of a target gene in a cell, by expressing in the cell an

CC expression cassette comprising a promoter operably linked to a sense or
CC antisense targeting sequence having substantial identity to a subsequence
CC of the target gene, and an inverted repeat (IR) of a subsequence of a NOS
CC (nopaline synthase) gene, where the IR is unrelated to the targeting
CC sequence. The expression cassette, pFP-IRN1 is constructed using a
CC figwort mosaic virus (FMV) promoter in which the 5'-untranslated leader
CC (5'-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato
CC polygalacturonase (PG) gene and an IR of the terminator of the
CC Agrobacterium tumefaciens NOS gene. The method is useful for regulating
CC expression of endogenous genes and transgenes, e.g. to regulate
CC expression of endogenous plant phenotypes, such as disease resistance,
CC flavour, protein or nutritional characteristics. The improved gene
CC silencing construct is used in functional genomics to determine the
CC effect of regulating gene expression of a selected endogenous gene or
CC transgene. The method is simple and rapid, and is suitable for high-
CC throughput studies. Multiple transgenic constructs all containing the
CC same repeat element can be silenced at the same time, since the initial
CC silencing trigger mediated through the inverted repeat region will apply
CC to all of the transcripts. The present sequence represents the expression
CC cassette, pFP-IRN1
XX

1 SQ Sequence 5822 BP; 1689 A; 1275 C; 1292 G; 1566 T; 0 U; 0 Other;

Query Match 100.0%; Score 5822; DB 6; Length 5822;
Best local Similarity 100.0%; Pred. No. 0;
Matches 5822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGCAGCAGGTTTCCCGACCTGGAAAGCGGCGAGTGAGCGCAACCAATTAAATGTGAG 60
DB 1 CTGGCAGCAGGTTTCCCGACCTGGAAAGCGGCGAGTGAGCGCAACCAATTAAATGTGAG 60
QY 61 TTAGCTCAGCTCATTTAGGACGCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTG 120
DB 61 TTAGCTCAGCTCATTTAGGACGCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTG 120
QY 121 TGGAAATGTGAGCGGATACAAATTTTACAGGAAACAGCTATGACCATGATTTACGCCAA 180
DB 121 TGGAAATGTGAGCGGATACAAATTTTACAGGAAACAGCTATGACCATGATTTACGCCAA 180
QY 181 GCTATTAGGTGACACTATAGATCTCAAGCTATGCTCAACGCGTTGGAGCTCTCC 240
DB 181 GCTATTAGGTGACACTATAGATCTCAAGCTATGCTCAACGCGTTGGAGCTCTCC 240
QY 241 CATATGCTGACCTGCAGCGCGCGCACTAGTGATGCTTAGATCTCGAGTGGAGCTAAT 300
DB 241 CATATGCTGACCTGCAGCGCGCGCACTAGTGATGCTTAGATCTCGAGTGGAGCTAAT 300
QY 301 TCTCAGTCCAAAGCCTCAACAAGTCAAGGTACAGGTCTCCAAACCAATTAGCCAAAGC 360
DB 301 TCTCAGTCCAAAGCCTCAACAAGTCAAGGTACAGGTCTCCAAACCAATTAGCCAAAGC 360
QY 361 TACAGGAGATCAATGAAGAATCTTCAATCAAAGTAAACTACTGTTCCAGCACATGCATCA 420
DB 361 TACAGGAGATCAATGAAGAATCTTCAATCAAAGTAAACTACTGTTCCAGCACATGCATCA 420
QY 421 TGGTCACTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCTTTG 480
DB 421 TGGTCACTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCTTTG 480
QY 481 AAAGTAATCTTGTCAAATCGAGCAGCTGGCTGTGGGGACGACACAAAAAGGAATGGT 540
DB 481 AAAGTAATCTTGTCAAATCGAGCAGCTGGCTGTGGGGACGACACAAAAAGGAATGGT 540
QY 541 GCAGAAATGTTAGCGGCACCTTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAGCAG 600
DB 541 GCAGAAATGTTAGCGGCACCTTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAGCAG 600
QY 601 ATTCCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGCTGACAGCCAC 660
DB 601 ATTCCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGCTGACAGCCAC 660
QY 661 TCACATAATGCGTATGACAAAGCGAGTGAACGACCAAAAGAAATTTAGCTTGAGCTCAGAT 720
DB 661 TCACATAATGCGTATGACAAAGCGAGTGAACGACCAAAAGAAATTTAGCTTGAGCTCAGAT 720

DB 661 TCACATAATGCGTATGACAAAGCGAGTGAACGACCAAAAGAAATTTAGCTTGAGCTCAGAT 720
QY 721 TTAGCAGCATTCAGAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTCAAA 780
DB 721 TTAGCAGCATTCAGAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTCAAA 780
QY 781 TTGGTATGCGCAAAACCAAGAAGAACTCCATCTCTCAAGAGTTTGTGAAGAAGAAATCT 840
DB 781 TTGGTATGCGCAAAACCAAGAAGAACTCCATCTCTCAAGAGTTTGTGAAGAAGAAATCT 840
QY 841 CAGTCCAAAGCCTCAACNAGTTCAGAGTTCAGAGTCTCCAAACCATTTAGCCAAAAGCTAC 900
DB 841 CAGTCCAAAGCCTCAACNAGTTCAGAGTTCAGAGTCTCCAAACCATTTAGCCAAAAGCTAC 900
QY 901 AGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCATCATG 960
DB 901 AGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCATCATG 960
QY 961 TCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCTTTGAAA 1020
DB 961 TCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCTTTGAAA 1020
QY 1021 GTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGAAATGGTGCA 1080
DB 1021 GTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGAAATGGTGCA 1080
QY 1081 GAATTTGTAGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAGCAGATT 1140
DB 1081 GAATTTGTAGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAGCAGATT 1140
QY 1141 CCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGTCTCTGACAGCCACCTCA 1200
DB 1141 CCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGTCTCTGACAGCCACCTCA 1200
QY 1201 CTAATCGTATGACGACGAGTACGACCAACAAAGAAATTCCTCTCTATATATAAGAGGCA 1260
DB 1201 CTAATCGTATGACGACGAGTACGACCAACAAAGAAATTCCTCTCTATATATAAGAGGCA 1260
QY 1261 TTCATTTCCCAATTTGAGGACACAGAAAAATTTGCTACATTTGTTTCACAAACTTCAAAATAT 1320
DB 1261 TTCATTTCCCAATTTGAGGACACAGAAAAATTTGCTACATTTGTTTCACAAACTTCAAAATAT 1320
QY 1321 TATTCAATTTATTTGTGACGCTTTCAAACTCTTTGTTTCTTCTGTTTGTGTTGATTTAGT 1380
DB 1321 TATTCAATTTATTTGTGACGCTTTCAAACTCTTTGTTTCTTCTGTTTGTGTTGATTTAGT 1380
QY 1381 AAAACCATGCTTCTCTAAAAACAAGAAATTAATCTTCTCAAGCAAAATCACTTTTCAGGTCCA 1440
DB 1381 AAAACCATGCTTCTCTAAAAACAAGAAATTAATCTTCTCAAGCAAAATCACTTTTCAGGTCCA 1440
QY 1441 TGCAGATCTTTCTATTTTCAGTAAAGATTTTGGATCTTTAGAGCATCTAGTAAATTTTCA 1500
DB 1441 TGCAGATCTTTCTATTTTCAGTAAAGATTTTGGATCTTTAGAGCATCTAGTAAATTTTCA 1500
QY 1501 GACTACAAAGATAGAGGCTTTGGATGCTTTTGTATGATGTTTCAAAATTTAGTTGTTGGA 1560
DB 1501 GACTACAAAGATAGAGGCTTTGGATGCTTTTGTATGATGTTTCAAAATTTAGTTGTTGGA 1560
QY 1561 GGAGGAGGAATCAATGCAAGTATGGTGGCCAAAGTCTCTGCAAAATAAAT 1620
DB 1561 GGAGGAGGAATCAATGCAAGTATGGTGGCCAAAGTCTCTGCAAAATAAAT 1620
QY 1621 AAATCACTGCGCATGAGGGATGCACCAACCGGCTTAACTTCTGGAATTTGCAAAAAATTTG 1680
DB 1621 AAATCACTGCGCATGAGGGATGCACCAACCGGCTTAACTTCTGGAATTTGCAAAAAATTTG 1680
QY 1681 AAAGTGAATTAATCTTAAGAGTAAATTCACAAATTCATATCAAAATTTGAGTCATGC 1740
DB 1681 AAAGTGAATTAATCTTAAGAGTAAATTCACAAATTCATATCAAAATTTGAGTCATGC 1740
QY 1741 ACTAATCTTGTAGCTTCAAAATTTGATGATCAATGCTTTCAGCAAAAGAGCCCAAAATCTGAT 1800
DB 1741 ACTAATCTTGTAGCTTCAAAATTTGATGATCAATGCTTTCAGCAAAAGAGCCCAAAATCTGAT 1800

1801 GGAGTCCATGATCAATACCTCAATATATTCAAATATCTGATATCTATTTGGAACAGGT 1860
1801 GGAGTCCATGATCAATACCTCAATATATTCAAATATCTGATATCTATTTGGAACAGGT 1860
1861 GATGATTGTATTTCAAATGTTTCTCGGATCTCAAATGTCAGGCGCAAAATATTTACTTGT 1920
1861 GATGATTGTATTTCAAATGTTTCTCGGATCTCAAATGTCAGGCGCAAAATATTTACTTGT 1920
1921 GGTCAGGTCATGTGATTAAGATTTGGAAGCTTAGGATCTGGAATTCAGAACTTATGTG 1980
1921 GGTCAGGTCATGTGATTAAGATTTGGAAGCTTAGGATCTGGAATTCAGAACTTATGTG 1980
1981 TCTAATGTTACTGTAATGAAGCCTTAAATATTCGGTCCGGAATGGAATGAGATCAAG 2040
1981 TCTAATGTTACTGTAATGAAGCCTTAAATATTCGGTCCGGAATGGAATGAGATCAAG 2040
2041 ACTTGGCAGGAGGATCTGGAACAGCTAGCAACATCAAATTTCTGAATGTGGAATGCAA 2100
2041 ACTTGGCAGGAGGATCTGGAACAGCTAGCAACATCAAATTTCTGAATGTGGAATGCAA 2100
2101 GACGTTAAGTATCCCAATATATAGACCAAACTATTGTGATCGAGTTGAACCAATGATA 2160
2101 GACGTTAAGTATCCCAATATATAGACCAAACTATTGTGATCGAGTTGAACCAATGATA 2160
2161 CAACAGTTTTCAGCAGTTCAAGTGAAATATGTTGTTGATGAGATATCAAGGCGACAGT 2220
2161 CAACAGTTTTCAGCAGTTCAAGTGAAATATGTTGTTGATGAGATATCAAGGCGACAGT 2220
2221 GCAACAAAGTGCGCATAAATTTGATTGACGACAAACTTTCCATGTGAAGGAATATA 2280
2221 GCAACAAAGTGCGCATAAATTTGATTGACGACAAACTTTCCATGTGAAGGAATATA 2280
2281 ATGAGAAATATAAATTTAGTAGGGAAGTGGAAGAACATCAGAGGCTTACGTGCAAAAT 2340
2281 ATGAGAAATATAAATTTAGTAGGGAAGTGGAAGAACATCAGAGGCTTACGTGCAAAAT 2340
2341 GTCCATTTTAAACATGCTGAACATGTTACACCACTGCATCTCACTAGAAATTTTCAGAG 2400
2341 GTCCATTTTAAACATGCTGAACATGTTACACCACTGCATCTCACTAGAAATTTTCAGAG 2400
2401 GATGAAGCTCTTTTGTATTAATTAATCTCGAGTCGATCTAGTAAACATAGATGACACC 2460
2401 GATGAAGCTCTTTTGTATTAATTAATCTCGAGTCGATCTAGTAAACATAGATGACACC 2460
2461 GCGCGGATTAATTTATCTAGTTTGGCGCTATATTTTGTGTTCTATCGCGTATTAATGT 2520
2461 GCGCGGATTAATTTATCTAGTTTGGCGCTATATTTTGTGTTCTATCGCGTATTAATGT 2520
2521 ATAAATCGGGACTCTAATCAGAAAAACCCATCTCATAAATAACGTCAATGATTAACATGT 2580
2521 ATAAATCGGGACTCTAATCAGAAAAACCCATCTCATAAATAACGTCAATGATTAACATGT 2580
2581 TAATTAATACATGCTTAACGTAATTAACAGAAATTAATGATTAATCAATCGCAAGACCGG 2640
2581 TAATTAATACATGCTTAACGTAATTAACAGAAATTAATGATTAATCAATCGCAAGACCGG 2640
2641 CAACAGGATTCATCTTAAGAAACTTTATTCGCAAACTTTTGAACATCTGCTGACTCTA 2700
2641 CAACAGGATTCATCTTAAGAAACTTTATTCGCAAACTTTTGAACATCTGCTGACTCTA 2700
2701 GAGGATCTCAATTTTACTGTGAACATTTCTGCTCAATTTGACCAATCAAGCGGTACGG 2760
2701 GAGGATCTCAATTTTACTGTGAACATTTCTGCTCAATTTGACCAATCAAGCGGTACGG 2760
2761 TTGTTTCGTTAAATGTGAAATTAATTTGCTTCTATTTGACCAATCAAGCGGTACGG 2820
2761 TTGTTTCGTTAAATGTGAAATTAATTTGCTTCTATTTGACCAATCAAGCGGTACGG 2820
2821 ATCTTCTAGAGTCAAGCAGATCGTTCAAACTTTGCAAACTTTGCAAACTTTGCAAACTTTG 2880
2821 ATCTTCTAGAGTCAAGCAGATCGTTCAAACTTTGCAAACTTTGCAAACTTTGCAAACTTTG 2880

2881 TCCGTTGCGGCTCTCGGATGATTATCATATAATTTCTGTTGAATTTACGTTAAGCATGT 2940
2881 TCCGTTGCGGCTCTCGGATGATTATCATATAATTTCTGTTGAATTTACGTTAAGCATGT 2940
2941 AATAAATTAACATGTAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
2941 AATAAATTAACATGTAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
3001 GCAATTAATTAATTAACGATAGAAAAAATAATAGCGGCAAACTAGGATAAAT 3060
3001 GCAATTAATTAATTAACGATAGAAAAAATAATAGCGGCAAACTAGGATAAAT 3060
3061 ATCGCGCGGCTGTCATCTATGTTACTAGATCGACCTGACGATGAGATGAGATGAGATGAG 3120
3061 ATCGCGCGGCTGTCATCTATGTTACTAGATCGACCTGACGATGAGATGAGATGAGATGAG 3120
3121 ATCGAGCTCGGCGCAATTTGCGCTATAGTAGTCTGATTAATTAATTAATTAATTAATTAAT 3180
3121 ATCGAGCTCGGCGCAATTTGCGCTATAGTAGTCTGATTAATTAATTAATTAATTAATTAAT 3180
3181 TTTACAACGCTGCTGACCTGGGAAACCCCTGGGTTACCCAACTTAATGCTTGCAGACACA 3240
3181 TTTACAACGCTGCTGACCTGGGAAACCCCTGGGTTACCCAACTTAATGCTTGCAGACACA 3240
3241 TCCGCTTTTCGCGAGCTGCGTAATAGCAAGAGCGCGCACCGATCGCCCTTCCCAACA 3300
3241 TCCGCTTTTCGCGAGCTGCGTAATAGCAAGAGCGCGCACCGATCGCCCTTCCCAACA 3300
3301 GTTTCGCGAGCTGAAATGGCGAATGGAGCGCGCTGTAGCGCGCATTAAGCGCGCGGCT 3360
3301 GTTTCGCGAGCTGAAATGGCGAATGGAGCGCGCTGTAGCGCGCATTAAGCGCGCGGCT 3360
3361 GTGCTGTTAGCGCAGCTGACCGCTACACTTCCGAGCGCCCTAGCGCGGCTTCCCTTTC 3420
3361 GTGCTGTTAGCGCAGCTGACCGCTACACTTCCGAGCGCCCTAGCGCGGCTTCCCTTTC 3420
3421 GCTTCTTCCCTTCTCGCCACGCTGCGCGGCTTCCGCGCTCAAGCTCTAAATCGG 3480
3421 GCTTCTTCCCTTCTCGCCACGCTGCGCGGCTTCCGCGCTCAAGCTCTAAATCGG 3480
3481 GGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTTACGGCACCTTCGACCGCAAAACTTGTAT 3540
3481 GGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTTACGGCACCTTCGACCGCAAAACTTGTAT 3540
3541 TTGGTGATGTTGTCAGTAGTGGGCAATCGCCCTGATAGAGGTTTTCGCGCTTTGAG 3600
3541 TTGGTGATGTTGTCAGTAGTGGGCAATCGCCCTGATAGAGGTTTTCGCGCTTTGAG 3600
3601 TTGGAGTCCAGTCTTTTAAATAGTGGACTCTTGTTCAAACTGGAACAACACTCAACCT 3660
3601 TTGGAGTCCAGTCTTTTAAATAGTGGACTCTTGTTCAAACTGGAACAACACTCAACCT 3660
3661 ATCTCGGCTTATCTTTTGAATTAAGGGATTTTTCGCGATTTTCGCGCTATTTGGTTAAAA 3720
3661 ATCTCGGCTTATCTTTTGAATTAAGGGATTTTTCGCGATTTTTCGCGCTATTTGGTTAAAA 3720
3721 AATGAGCTGATTTAAACAAATTTTAAACGGAATTTTAAACAAATTTTAAACGCTTACAAAT 3780
3721 AATGAGCTGATTTAAACAAATTTTAAACGGAATTTTAAACAAATTTTAAACGCTTACAAAT 3780
3781 TCGGCTGATCGGTTATTTCTCTTACGATCTGCGGTTATTTTCAACCGCATACAGGT 3840
3781 TCGGCTGATCGGTTATTTCTCTTACGATCTGCGGTTATTTTCAACCGCATACAGGT 3840
3841 GGCACCTTTTCGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCA 3900
3841 GGCACCTTTTCGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCA 3900
3901 AATATGATCGGCTCATGAGACAAATACCCCTGATAAATGCTTCAATTAATTTGAAAAAGG 3960
3901 AATATGATCGGCTCATGAGACAAATACCCCTGATAAATGCTTCAATTAATTTGAAAAAGG 3960
3961 AAGAGTATGAGTATTCACATTTTCGCTGTCGCGCTTATTCCTTTTTCGCGCATTTTTCG 4020

PD 09-AUG-1996.
 XX PF 24-MAY-1995; 95CA-02150039.
 XX PR 08-FEB-1995; 95GB-00002456.
 XX XX (UYWA-) UNIV WARWICK.
 XX PI Bennett M, May S, Ramsay N;
 XX DR WPI; 1996-486150/49.
 XX PT Control of genes in transgenic plants - using an upstream activating
 PT sequence activated by a transactivating protein expressed using a
 PT separate promoter.
 XX ES Example; Fig 5F; 48pp; English.
 XX
 CC Reporter plasmid pUMIGIT (AAT43137), or pUAS Minimal promoter Gus Int
 CC terminator, contains a beta-glucuronidase (GUS) reporter gene under the
 CC control of the 46S cauliflower-mosaic virus minimal promoter and 10
 CC synthetic 17-bp GAL4 binding sites. The upstream activating sequence
 CC (UAS) of pUMIGIT is activatable by yeast transactivating protein GAL4. In
 CC a novel method for controlling gene expression, a first transgenic plant
 CC carrying a gene encoding a desired phenotype (herbicide resistance of
 CC polyhydroxybutyrate prodn.) operatively linked to a UAS recognition site
 CC is pollinated by a second transgenic plant carrying Gal4 DNA (see also
 CC AAT43136). The transgene is fully expressed in F1 hybrid plants but
 CC segregates apart in subsequent generations, improving environmental
 CC safety
 XX SQ Sequence 5534 BP; 1400 A; 1355 C; 1367 G; 1363 T; 0 U; 29 Other;
 Query Match 47.4%; Score 2757.2; DB 2; Length 5534;
 Best Local Similarity 96.3%; Pred. No. 0;
 Matches 2891; Conservative 0; Mismatches 37; Indels 74; Gaps 4;
 QY 2840 GATCGTTCAACACATTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTTCGCG 2899
 DB 2366 GATCGTTCAACACATTGGCAATAAAGTTCTTAAGATTGAATCCTGTGCGGCTTCGCG 2425
 QY 2300 ATGATTATCATATAATTTCTGTTGAATTTACGTTAAGCATGTAATAATTAACATGTAATGC 2959
 DB 2426 ATGATTATCATATAATTTCTGTTGAATTTACGTTAAGCATGTAATAATTAACATGTAATGC 2485
 QY 2360 ATGACGTTATTTATGAGATGGTTTTTATGATTAGATCCCGCAATTATACATTTAATAC 3019
 DB 2486 ATGACGTTATTTATGAGATGGTTTTTATGATTAGATCCCGCAATTATACATTTAATAC 2545
 QY 3020 GCGATAGAAAAAATAATAGCGGCAAACTAGGATTAATTTATCGGCGGCTGTCATCT 3079
 DB 2546 GCGATAGAAAAAATAATAGCGGCAAACTAGGATTAATTTATCGGCGGCTGTCATCT 2605
 QY 3080 ATGTTACTAGATCGAAC-----TGCAGGSCATGGGATCGCGCGCGCATGC 3124
 DB 2606 ATGTTACTAGATCANNNGAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGACGGG 2665
 QY 3125 GACGTGCGGCCCAATTGCGCCCTATAGTGAATCGTATTTAC-----AATTCTAGCGCGTGT 3181
 DB 2666 GGCCCGGTATCCCAATTGCGCCCTATAGTGAATCGTATTTACGCGCGCTCACTGGCGGTGTT 2725
 QY 3182 TTCAACGTCGTGATCGGAAAAACCTGGCGCTTACCGCACTTAATTCGCTTGCAGCACAT 3241
 DB 2726 TTCAACGTCGTGATCGGAAAAACCTGGCGCTTACCGCACTTAATTCGCTTGCAGCACAT 2785
 QY 3242 CCCCTTTGCGCAGTGGCGTAATAGGAGAGGCGCCGCAACCGATCGCCCTTCCCAACAG 3301
 DB 2786 CCCCTTTGCGCAGTGGCGTAATAGGAGAGGCGCCGCAACCGATCGCCCTTCCCAACAG 2845
 QY 3302 TTGCGCAGCTGAATGGCGAAT-GGACGCGCCTGTAGCGCGCAATTAAAGCGCGCGGGT 3360
 DB 2846 TTGCGCAGCTGAATGGCGAATGGACGCGCCTGTAGCGCGCAATTAAAGCGCGCGGGT 2905
 QY 3361 GTGGTGGTTAGCGCAGCGTGACCGCTACACTTGCAGGCGCCTAGCGCGCCTCTCTTTC 3420
 DB 2906 GTGGTGGTTAGCGCAGCGTGACCGCTACACTTGCAGGCGCCTAGCGCGCCTCTCTTTC 2965
 QY 3421 GCTTTCTTCCCTTCTCTCGCCACAGTTTCGCGGCTTTCGCGGCTCAAGCTCTAATAATCGG 3480
 DB 2966 GCTTTCTTCCCTTCTCTCGCCACAGTTTCGCGGCTTTCGCGGCTCAAGCTCTAATAATCGG 3025
 QY 3481 GGGCTCCCTTTAGGTTCCGATTAGACTTTACGGCACCTCGACCGCAAAAACCTGAT 3540
 DB 3026 GGGCTCCCTTTAGGTTCCGATTAGACTTTACGGCACCTCGACCGCAAAAACCTGAT 3085
 QY 3541 TTGGGTGATGCTTACGCTAGTGGGCCATCGCCCTGATAGAGCGTTTTCGCGCCTTTCGACG 3600
 DB 3086 TAGGTGATGCTTACGCTAGTGGGCCATCGCCCTGATAGAGCGTTTTCGCGCCTTTCGACG 3145
 QY 3601 TTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACCAACACTCAACCT 3660
 DB 3146 TTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACCAACACTCAACCT 3205
 QY 3661 ATCTCGGCTATCTCTTTGATTATAGGGAATTTGCGGATTCGCGCTATTTGGTTAAAA 3720
 DB 3206 ATCTCGGCTATCTCTTTGATTATAGGGAATTTGCGGATTTGCGGCTATTTGGTTAAAA 3265
 QY 3721 AATGAGCTGATTAAACAAATATTTAAACGCGAATTTTAAACAAATATTTAAACGTTACAAT 3780
 DB 3266 AATGAGCTGATTAAACAAATATTTAAACGCGAATTTTAAACAAATATTTAAACGTTACAAT 3325
 QY 3781 TCGGCTGATGCGGTATTTCTCTCTTACGCACTCTGCGGTATTTTACACCGCATACAGT 3840
 DB 3326 T-----AGT 3330
 QY 3841 GGCACCTTTTCGGGAAATGTCGCGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCA 3900
 DB 3331 GGCACCTTTTCGGGAAATGTCGCGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCA 3390
 QY 3901 AATATGATCGCTCATGAGACAATAACCCGTAATAATGCTTCAATATATTTGAAAAAGG 3960
 DB 3391 AATATGATCGCTCATGAGACAATAACCCGTAATAATGCTTCAATATATTTGAAAAAGG 3450
 QY 3961 AAGAGTATGAGTATTTCAACATTTCCGTGTCGCGCTTATTCCTTTTTCGGGCAATTTTCG 4020
 DB 3451 AAGAGTATGAGTATTTCAACATTTCCGTGTCGCGCTTATTCCTTTTTCGGGCAATTTTCG 3510
 QY 4021 CTTCTCTGTTTTCCTACCCAGAAACCGTGGTGAAAGTAAAGATGCTGAAGATCAGTTG 4080
 DB 3511 CTTCTCTGTTTTCCTACCCAGAAACCGTGGTGAAAGTAAAGATGCTGAAGATCAGTTG 3570
 QY 4081 GGTGCACGAGTGGGTTCATCGAACTGATCTCAACAGCGGTAAGATCTCTTGAGAGTTT 4140
 DB 3571 GGTGCACGAGTGGGTTCATCGAACTGATCTCAACAGCGGTAAGATCTCTTGAGAGTTT 3630
 QY 4141 CGCCCCGAAGAACCTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGCTA 4200
 DB 3631 CGCCCCGAAGAACCTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGCTA 3690
 QY 4201 TTATCCCGTATTTAGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAA 4260
 DB 3691 TTATCCCGTATTTAGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAA 3750
 QY 4261 GACTTGGTTGAGTACTCACCAGTACAGAAAGGATCTTACGAGTGCATGACAGTAAGA 4320
 DB 3751 GACTTGGTTGAGTACTCACCAGTACAGAAAGGATCTTACGAGTGCATGACAGTAAGA 3810
 QY 4321 GAATTATGCACTGCTGCGCATAACCATGAGTGATAACTGCGGCAACTTCTTCTGACA 4380
 DB 3811 GAATTATGCACTGCTGCGCATAACCATGAGTGATAACTGCGGCAACTTCTTCTGACA 3870
 QY 4381 ACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTCACAACTATGCGGAGTCAATGTAAC 4440
 DB 3871 ACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTCACAACTATGCGGAGTCAATGTAAC 3930
 QY 4441 CGCCTTTCATGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACC 4500

Db 3931 CGCCTTGATCGTTGGGAAACCGAGCTCAATGAAGCCATACCAACACGACGAGCTGACACC 3990
Qy 4501 ACCATGCTGTAGCAATGGCAACAAAGCTTCGGCAAACTATTAACTGCGGAACCTACTTACT 4560
Db 3991 ACCATGCTGTAGCAATGGCAACAAAGCTTCGGCAAACTATTAACTGCGGAACCTACTTACT 4950
Qy 4561 CTAGCTTCCCGGCAACAAATTAATAGACTGGAGCGGATAAAGTTGACGACCACTT 4620
Db 4051 CTAGCTTCCCGGCAACAAATTAATAGACTGGAGCGGATAAAGTTGACGACCACTT 4110
Qy 4621 CTGCGCTCGGCCCTTCGGCTGGCTGCTTTATTTGCTGATAAATCTGGAGCGGTGAGCGT 4680
Db 4111 CTGCGCTCGGCCCTTCGGCTGGCTGCTTTATTTGCTGATAAATCTGGAGCGGTGAGCGT 4170
Qy 4681 GGGTCTCGCGGTATCATTTGACGACCTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT 4740
Db 4171 GGGTCTCGCGGTATCATTTGACGACCTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT 4230
Qy 4741 ATCTACACGACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATA 4800
Db 4231 ATCTACACGACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATA 4290
Qy 4801 GGTGCTCACTGATTAAAGATTTGGTAATCTGTACAGCAAGTTTACTCATATATCTTTAG 4860
Db 4291 GGTGCTCACTGATTAAAGATTTGGTAATCTGTACAGCAAGTTTACTCATATATCTTTAG 4350
Qy 4861 ATTGATTTAAACCTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTATAAT 4920
Db 4351 ATTGATTTAAACCTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTATAAT 4410
Qy 4921 CTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCACCTGAGCGTCAGACCCCGTAGAA 4980
Db 4411 CTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCACCTGAGCGTCAGACCCCGTAGAA 4470
Qy 4981 AAGATCAAGGATCTTCTGAGATCCTTTTTCGTGCGGTAACTCTGCTGCTGCAACA 5040
Db 4471 AAGATCAAGGATCTTCTGAGATCCTTTTTCGTGCGGTAACTCTGCTGCTGCAACA 4530
Qy 5041 AAAAAACACCGCTTACAGCGGTGCTTTTTCGTGCGGTAACTCTGCTGCTGCAACA 5100
Db 4531 AAAAAACACCGCTTACAGCGGTGCTTTTTCGTGCGGTAACTCTGCTGCTGCAACA 4590
Qy 5101 CCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATCTGCTTCTAGTGTAGCCG 5160
Db 4591 CCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATCTGCTTCTAGTGTAGCCG 4650
Qy 5161 TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCTGCTGCTAATC 5220
Db 4651 TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCTGCTGCTAATC 4710
Qy 5221 CTGTTACAGTGGCTGCTGCGAGTGGGATGAAGTCTGCTTACCGGGTTGGACTCAAGA 5280
Db 4711 CTGTTACAGTGGCTGCTGCGAGTGGGATGAAGTCTGCTTACCGGGTTGGACTCAAGA 4770
Qy 5281 CGATAGTTACGGATAAGCGCAGCGTTCGGGTGAAACGGGGGTTTCGTGACACAGCC 5340
Db 4771 CGATAGTTACGGATAAGCGCAGCGTTCGGGTGAAACGGGGGTTTCGTGACACAGCC 4830
Qy 5341 AGCTTGGAGCGAAGCACTACCGAAGTCAAGATACCTACAGCGTGAAGTATGAGAAC 5400
Db 4831 AGCTTGGAGCGAAGCACTACCGAAGTCAAGATACCTACAGCGTGAAGTATGAGAAC 4890
Qy 5401 GCCACGCTTCCCGAAGCGAAGGAGGACAGGTATCCGGTAAAGCGGAGGTTCGGAACA 5460
Db 4891 GCCACGCTTCCCGAAGCGAAGGAGGACAGGTATCCGGTAAAGCGGAGGTTCGGAACA 4950
Qy 5461 GGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCCCTGGTATCTTTTATGCTTCGCGG 5520
Db 4951 GGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCCCTGGTATCTTTTATGCTTCGCGG 5010
Qy 5521 TTTTCGCCACCTCTGACTTGAGCTGCAATTTTGTGATGCTCTGTCAGGGGGCGAGCCTA 5580

Db 5011 TTTTCGCCACCTCTGACTTGTAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTA 5070
Qy 5581 TGGAAAAACGCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGTGCTGCTTTTGT 5640
Db 5071 TGGAAAAACGCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGTGCTGCTTTGCT 5130
Qy 5641 CACATGTTCTTCTCCTCGTTATCCCTGATCTCTGTGATAAACCGTATACCGCTTTGAG 5700
Db 5131 CACATGTTCTTCTCCTCGTTATCCCTGATCTCTGTGATAAACCGTATACCGCTTTGAG 5190
Qy 5701 TGAGCTGTATACCTCGCCGACCGCAACGACCGAGCGAGTCAGTGACGAGGAA 5760
Db 5191 TGAGCTGTATACCTCGCCGACCGCAACGACCGAGCGAGTCAGTGACGAGGAA 5250
Qy 5761 GCGGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTGGCGGATTCATTAATGC 5820
Db 5251 GCGGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTGGCGGATTCATTAATGC 5310
Qy 5821 AG 5822
Db 5311 AG 5312

RESULT 3
AAH25896/c
ID AAH25896 standard; DNA; 4229 BP.
XX
AC AAH25896;
XX
DT 24-AUG-2001 (first entry)
XX
DE Genetic information stability related oligonucleotide #5.
XX
KW Genetic information stability measurement; drug resistance; ds.
XX
OS Synthetic.
XX
PN JP2001087000-A.
XX
PD 03-APR-2001.
XX
PF 17-SEP-1999; 99JP-00264320.
XX
PR 17-SEP-1999; 99JP-00264320.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KX.
XX
DR WPI; 2001-360322/38.
XX
PT Measurement of stability of genetic information in an animal cell,
PT comprises introducing a vector having a gene resistant to a first drug
PT and a gene sensitive to a second drug, to an animal cell.
XX
PS Disclosure; Page 8-9; 12pp; Japanese.
XX
CC The present invention describes a method for the measurement of stability
CC of genetic information in an animal cell in which a vector having a gene
CC resistant to a first drug and a gene sensitive to a second drug is
CC introduced into the animal cell. This can be used for the measurement of
CC stability of genetic information in an animal cell. The present sequence
CC is an oligonucleotide used in the exemplification of the invention
XX
SQ Sequence 4229 BP; 1108 A; 1004 C; 1036 G; 1081 T; 0 U; 0 Other;
Query Match 46.1%; Score 2686; DB 4; Length 4229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3137 AATTCGCCCTATAGTGTAGTGTATTAACAATCACTGCGCGTGTGTTTACACGTCGTGAC 3196
Db 3157 AATTCGCCCTATAGTGTAGTGTATTAACAATCACTGCGCGTGTGTTTACACGTCGTGAC 3098
Qy 3197 TGGAAAAACCTGCGGTATACCAACTTAATCGCTTCGACACATCCCCCTTCCGCCAGC 3256

Db	3097		TGGGAAACCTGGGGTACCCAACTTAATCGCTTGAGACACATCCCCCTTCCGACG	3038
QY	3257		TGGCGTAATAGGAAGAGCGCGCACCGATGCCCTTCCCAACAGTTGCGCAGCCTGAAT	3316
Db	3037		TGGCGTAATAGGAAGAGCGCGCACCGATGCCCTTCCCAACAGTTGCGCAGCCTGAAT	2978
QY	3317		GGCGAATCGAGCGCGCTGTAGCGCGCATTAAGCGCGCGCGGGTGTGTGTTACGCGCA	3376
Db	2977		GGCGAATCGAGCGCGCTGTAGCGCGCATTAAGCGCGCGCGGGTGTGTGTTACGCGCA	2918
QY	3377		CGGTGACCGCTACACTTGGCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCCCTTCT	3436
Db	2917		CGGTGACCGCTACACTTGGCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCCCTTCT	2858
QY	3437		TTCTCGCCACGTTGCGCGCTTTCGCGTCAAGCTCTAAATCGGGGCTCCCTTTAGGGT	3496
Db	2857		TTCTCGCCACGTTGCGCGCTTTCGCGTCAAGCTCTAAATCGGGGCTCCCTTTAGGGT	2798
QY	3497		TCCGATTTAGAGCTTACGGCACCTCGACCGCAAAACTTGAATTTGGGTGATGTTTAC	3556
Db	2797		TCCGATTTAGAGCTTACGGCACCTCGACCGCAAAACTTGAATTTGGGTGATGTTTAC	2738
QY	3557		GTAGTGGCCATCGCCCTGATAGCGGTTTTTGGCCCTTTGACGTTGGAGTCCACGTTCT	3616
Db	2737		GTAGTGGCCATCGCCCTGATAGCGGTTTTTGGCCCTTTGACGTTGGAGTCCACGTTCT	2678
QY	3617		TTAATAGTGAACCTTTGTTTCAAACTGGAACAACACTCAACCCCTATCTCGGTCTATTCT	3676
Db	2677		TTAATAGTGAACCTTTGTTTCAAACTGGAACAACACTCAACCCCTATCTCGGTCTATTCT	2618
QY	3677		TTGATTTAAGGATTTTGGCGATTTTCGGCTATTGGTTAAATAAGCTGATTTAAC	3736
Db	2617		TTGATTTAAGGATTTTGGCGATTTTCGGCTATTGGTTAAATAAGCTGATTTAAC	2558
QY	3737		AAATATTTAAGCGAAATTTTAAACAAATATTAACGTTTACAAATTCGGCTGATCGGTAT	3796
Db	2557		AAATATTTAAGCGAAATTTTAAACAAATATTAACGTTTACAAATTCGGCTGATCGGTAT	2498
QY	3797		TTTCTCCTTACGATCTGTGCGGTATTTCAACCGCATACAGGTGGCACTTTTCGGGAA	3856
Db	2497		TTTCTCCTTACGATCTGTGCGGTATTTCAACCGCATACAGGTGGCACTTTTCGGGAA	2438
QY	3857		ATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATTCGGCTCA	3916
Db	2437		ATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATTCGGCTCA	2378
QY	3917		TGAGACAATAACCCCTGATAAATGCTTCAATAATTGAAAAGGAAGATATGATATTC	3976
Db	2377		TGAGACAATAACCCCTGATAAATGCTTCAATAATTGAAAAGGAAGATATGATATTC	2318
QY	3977		AACATTTCCGTGCGCCCTATTCCCTTTTGGGCAATTTGCTTCCCTTTTGGCTC	4036
Db	2317		AACATTTCCGTGCGCCCTATTCCCTTTTGGGCAATTTGCTTCCCTTTTGGCTC	2258
QY	4037		ACCAGAAACCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACAGTGGGT	4096
Db	2257		ACCAGAAACCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACAGTGGGT	2198
QY	4097		ACATCGAACTGGATCTCAACAGCGTAAAGATCCTTGAGAGTTTTCGCCCGCAAGACGTT	4156
Db	2197		ACATCGAACTGGATCTCAACAGCGTAAAGATCCTTGAGAGTTTTCGCCCGCAAGACGTT	2138
QY	4157		TTCAATGATGAGCACTTTTAAAGTTCTGATGTTGGCGCGGTATTAATCCGCTATTGACG	4216
Db	2137		TTCAATGATGAGCACTTTTAAAGTTCTGATGTTGGCGCGGTATTAATCCGCTATTGACG	2078
QY	4217		CGGGCAGAGCACTCGGTGCGCGCATACACTATTCTCAAGATGACTTGGTTGAGTACT	4276
Db	2077		CGGGCAGAGCACTCGGTGCGCGCATACACTATTCTCAAGATGACTTGGTTGAGTACT	2018
QY	4277		CACAGTCACAGAAAGCATCTTACGGATGTCATGACAGTAAAGATATGCAATGCTG	4336

Db	2017		CACAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATTCAGTGTCTG	1958
QY	4337		COATAACCATGAGTGAATAACACTGCGGCAACTTACTTCTGCAACGATCGGAGACCGA	4396
Db	1957		COATAACCATGAGTGAATAACACTGCGGCAACTTACTTCTGCAACGATCGGAGACCGA	1898
QY	4397		AGGAGCTAACCGCTTTTTCGACAACTGCGGGGATCATGTAACTGCTTGTGCTGGG	4456
Db	1897		AGGAGCTAACCGCTTTTTCGACAACTGCGGGGATCATGTAACTGCTTGTGCTGGG	1838
QY	4457		AACCGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACACGATGCTGTAGCAA	4516
Db	1837		AACCGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACACGATGCTGTAGCAA	1778
QY	4517		TGGCAACAACTGTCGCAAACTATTAACTGCGAACTACTTACTCTAGCTTCCCGCAAC	4576
Db	1777		TGGCAACAACTGTCGCAAACTATTAACTGCGAACTACTTACTCTAGCTTCCCGCAAC	1718
QY	4577		AATTAATAGACTGGATGGAGGGGATAAAGTTGACGACCACTTCTGCTCGGCCCTTC	4636
Db	1717		AATTAATAGACTGGATGGAGGGGATAAAGTTGACGACCACTTCTGCTCGGCCCTTC	1658
QY	4637		CGGCTGGCTGTTTATCTGATAAATCTGAGCGCGTGAGCGTGGGTCTCGCGGTATCA	4696
Db	1657		CGGCTGGCTGTTTATCTGATAAATCTGAGCGCGTGAGCGTGGGTCTCGCGGTATCA	1598
QY	4697		TTGACGACTGGGCGAGATGGTAAGCCCTCCGCTATCTAGTTATCTACAGCGGGA	4756
Db	1597		TTGACGACTGGGCGAGATGGTAAGCCCTCCGCTATCTAGTTATCTACAGCGGGA	1538
QY	4757		GTCAGGCAACTATGGTAAGCAAGATAGACAGATCGCTGAGATAGTGCCTCAGTGATTA	4816
Db	1537		GTCAGGCAACTATGGTAAGCAAGATAGACAGATCGCTGAGATAGTGCCTCAGTGATTA	1478
QY	4817		AGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATATCTTATAGATTAAATCTTC	4876
Db	1477		AGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATATCTTATAGATTAAATCTTC	1418
QY	4877		ATTTTTAATTTAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCC	4936
Db	1417		ATTTTTAATTTAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCC	1358
QY	4937		CTTAACGTGAGTTTCTGTCACAGGCTCAGACCCCGTGAAGATCAAGATCTT	4996
Db	1357		CTTAACGTGAGTTTCTGTCACAGGCTCAGACCCCGTGAAGATCAAGATCTT	1298
QY	4997		CTTGAGATCCTTTTTTCTGCGGTATCTGCTGCTTGCAAAACAAACCAACCGCTAC	5056
Db	1297		CTTGAGATCCTTTTTTCTGCGGTATCTGCTGCTTGCAAAACAAACCAACCGCTAC	1238
QY	5057		CAGCGTGGTGTGTTTTCGGGATCAAGAGCTACCAACTCTTTTTCCGAAGTAACTGGCT	5116
Db	1237		CAGCGTGGTGTGTTTTCGGGATCAAGAGCTACCAACTCTTTTTCCGAAGTAACTGGCT	1178
QY	5117		TCAGCAGAGCGCATACCAAACTATCTCTTAGTGTAGCCGCTAGTTAGCCACCACT	5176
Db	1177		TCAGCAGAGCGCATACCAAACTATCTCTTAGTGTAGCCGCTAGTTAGCCACCACT	1118
QY	5177		TCAAGAACTCTGTAGCAGCGCTACATACCTCTGCTTCTGTAATCTGTTTACAGTGGCTG	5236
Db	1117		TCAAGAACTCTGTAGCAGCGCTACATACCTCTGCTTCTGTAATCTGTTTACAGTGGCTG	1058
QY	5237		CTGCCAGTGGCGATAAGTCTGTTTACCGGGTTGGAAGTCAAGACGATAGTTACCGGATA	5296
Db	1057		CTGCCAGTGGCGATAAGTCTGTTTACCGGGTTGGAAGTCAAGACGATAGTTACCGGATA	998
QY	5297		AGGCGCAGCGTGGGTGAAAGCGGGGTTCTGTCACACAGCCCGCTTGGAGCAACGA	5356
Db	997		AGGCGCAGCGTGGGTGAAAGCGGGGTTCTGTCACACAGCCCGCTTGGAGCAACGA	938
QY	5357		CCTACCGCACTGAGATACCTACAGCGTGTATGAGAAAGCGCCAGCTTCCCGAAG	5416
Db	937		CCTACCGCACTGAGATACCTACAGCGTGTATGAGAAAGCGCCAGCTTCCCGAAG	878

XX Unidentified.
XX WO200286101-A2.
XX
XX 31-OCT-2002.
XX
XX 24-APR-2002; 2002WO-BE000064.
XX
XX 24-APR-2001; 2001EP-00870088.
XX 17-JUL-2001; 2001US-0305604P.
XX (INNO-) INNOGENETICS NV.
XX
XX Depla E, Bosman A, Deschamps G, Sablon E, Suckow M, Samson I;
XX Verheyden G;
XX WPI; 2003-103409/09.
XX
XX New Hepatitis C virus (HCV) envelope protein with N-glycosylation
PT site(s), useful as a vaccine for inducing a HCV-specific immune response
PT or HCV-specific antibodies, particularly for preventing or treating HCV
PT infection.
XX
XX Example 1; Page 198-200; 355pp; English.
XX
XX The invention relates to Hepatitis C virus (HCV) envelope protein with N-
CC glycosylation site(s). The HCV envelope protein, or the pharmaceutical
CC composition comprising the envelope protein, is useful as a medicament or
CC a vaccine, particularly for inducing a HCV-specific immune response,
CC inducing HCV-specific antibodies or inducing a T-cell function in a
CC mammal. The protein is particularly useful for preventing, treating or
CC diagnosing HCV infection. It is also useful for detecting the presence of
CC anti-HCV antibodies in a sample. The present sequence is a vector DNA
CC used in the exemplification of the invention
XX
XX Sequence 3448 BP; 862 A; 883 C; 879 G; 824 T; 0 U; 0 Other;
XX
Query Match 46.1%; Score 2683.4; DB 7; Length 3448;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 3114 CGCGCGATCGAGCTGGGCCCAATTGCGCCCTATAGTAGTGGTATTAACAATCACTGG 3173
DB 2985 CGGGAGCATCGAGCTGGGCCCAATTGCGCCCTATAGTAGTGGTATTAACAATCACTGG 2926
QY 3174 CCCTCGTTTTACACGTCGTGACTGGGAAACCTCGCGTTACCCACTTAATCGCCTTG 3233
DB 2925 CCCTCGTTTTACACGTCGTGACTGGGAAACCTCGCGTTACCCACTTAATCGCCTTG 2866
QY 3234 CAGCACATCCCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTT 3293
DB 2865 CAGCACATCCCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTT 2806
QY 3294 CCCAACAGTTGCGAGCTGAATGGGGAATGAGACGCGCCCTGTAGCGGCGCATTAAGCGC 3353
DB 2805 CCCAACAGTTGCGAGCTGAATGGGGAATGAGACGCGCCCTGTAGCGGCGCATTAAGCGC 2746
QY 3354 GCGGGGTGTGTGTACGCGAGCTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGC 3413
DB 2745 GCGGGGTGTGTGTACGCGAGCTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGC 2686
QY 3414 TCCTTTTCGCTTTCTCCCTTTCCCTTTCTCGCCAGCTTCGCGGCTTTCCCGCTCAAGCTCT 3473
DB 2685 TCCTTTTCGCTTTCTCCCTTTCCCTTTCTCGCCAGCTTCGCGGCTTTCCCGCTCAAGCTCT 2626
QY 3474 AAATCGGGGCTCCCTTTAGGGTTCGATTAGAGCTTTACGCGACCTGACCGCAAAA 3533
DB 2625 AAATCGGGGCTCCCTTTAGGGTTCGATTAGAGCTTTACGCGACCTGACCGCAAAA 2566
QY 3534 ACTTGATTGGGTGATGTTACGTAGTGGGCCATCGCCCTGTAGACGCTTTTCGCCCC 3593
DB 2565 ACTTGATTGGGTGATGTTACGTAGTGGGCCATCGCCCTGTAGACGCTTTTCGCCCC 2506

QY 3594 TTTGAGCTTGGAGTCCACGTTCTTTAATAGTGACTCTTTTCCAAACTGGAACAACT 3653
DB 2505 TTTGAGCTTGGAGTCCACGTTCTTTAATAGTGACTCTTTTCCAAACTGGAACAACT 2446
QY 3654 CAACCCCTATCTCGGTCTATCTTTTGAATTAAGGGAATTTGCGGATTTTCGGCTATTG 3713
DB 2445 CAACCCCTATCTCGGTCTATCTTTTGAATTAAGGGAATTTGCGGATTTTCGGCTATTG 2386
QY 3714 GTTAAAAAATGAGCTGATTTTAAACAATATTTAACGGCAATTTTAAACAAATATTAAGCTT 3773
DB 2385 GTTAAAAAATGAGCTGATTTTAAACAATATTTAACGGCAATTTTAAACAAATATTAAGCTT 2326
QY 3774 TACAATTTCCGCTGATCGGCTATTTTCTCCTTACGCATCTGTGGGTATTTTCACCGCA 3833
DB 2325 TACAATTTCCGCTGATCGGCTATTTTCTCCTTACGCATCTGTGGGTATTTTCACCGCA 2266
QY 3834 TACAGTGGGACATTTTCGGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 3893
DB 2265 TACAGTGGGACATTTTCGGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 2206
QY 3894 ACATTTCAAAATATGATCTCGCTCATGAGACAATAAACCTGATAAATGCTTCAATAAATTTG 3953
DB 2205 ACATTTCAAAATATGATCTCGCTCATGAGACAATAAACCTGATAAATGCTTCAATAAATTTG 2146
QY 3954 AAAAAGGAAAGATGAGTATTCAACATTTCCGTGTGCGCCCTTATTTCCCTTTTTCGCGC 4013
DB 2145 AAAAAGGAAAGATGAGTATTCAACATTTCCGTGTGCGCCCTTATTTCCCTTTTTCGCGC 2086
QY 4014 ATTTTCCTTCTCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAGATGCTGAAGA 4073
DB 2085 ATTTTCCTTCTCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAGATGCTGAAGA 2026
QY 4074 TCAGTTGGGTGACGAGTGGGTTTACATCGAATCGAATCTCAACAGCGGTGAAGTCTCTTGA 4133
DB 2025 TCAGTTGGGTGACGAGTGGGTTTACATCGAATCTCAACAGCGGTGAAGTCTCTTGA 1966
QY 4134 GAGTTTTTCGCCCGGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTTG 4193
DB 1965 GAGTTTTTCGCCCGGAAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTTCA 1906
QY 4194 CGCGGTATTTATCCGCTATTGACGCGGGCAAGAGCAATCGCGTGGCGGCATACACTATTC 4253
DB 1905 TACACTATTTATCCGCTATTGACGCGGGCAAGAGCAATCGCGTGGCGGGCGGTATTC 1846
QY 4254 TCAGATGACTTGGTTGAGTACTACACAGTTCACAGAAAAGCATCTTACGATGGCATGAC 4313
DB 1845 TCAGATGACTTGGTTGAGTACTACACAGTTCACAGAAAAGCATCTTACGATGGCATGAC 1786
QY 4314 AGTAAGAGAAATTATGAGTGTCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACT 4373
DB 1785 AGTAAGAGAAATTATGAGTGTCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACT 1726
QY 4374 TCTGACAAAGATCGGAGGACGAGGAGCTTAACCGCTTTTTTTCACAACTATGGGGATCA 4433
DB 1725 TCTGACAAAGATCGGAGGACGAGGAGCTTAACCGCTTTTTTTCACAACTATGGGGATCA 1666
QY 4434 TGTAACCTCGCTTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACCGCAGCG 4493
DB 1665 TGTAACCTCGCTTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACCGCAGCG 1606
QY 4494 TGAACACGATGCTGTAGCAATGGCAACAGCTTTGCGCAAACTATTAATCTGCGCAACT 4553
DB 1605 TGAACACGATGCTGTAGCAATGGCAACAGCTTTGCGCAAACTATTAATCTGCGCAACT 1546
QY 4554 ACTTACTCTAGCTTCCCGGCAACAATTAAGTACTGATGAGGCGGATTAAGTTCCAGG 4613
DB 1545 ACTTACTCTAGCTTCCCGGCAACAATTAAGTACTGATGAGGCGGATTAAGTTCCAGG 1486
QY 4614 ACCACTTCTCGGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTCGAGCCGG 4673
DB 1485 ACCACTTCTCGGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTCGAGCCGG 1426

QY 4674 TGACGCTGGGTCCTCGCGGTATCATTTGACGACCTGGGGCCAGATGGTAAAGCCCTCCCGTAT 4733
Db |||||||
QY 1425 TGACGCTGGGTCCTCGCGGTATCATTTGACGACCTGGGGCCAGATGGTAAAGCCCTCCCGTAT 1366
Db |||||||
QY 4734 CGTAGTTATCTACACGACGGGAGTGCAGCAACTATGGATGAACGAAATAGACAGATGCG 4793
Db |||||||
QY 1365 CGTAGTTATCTACACGACGGGAGTGCAGCAACTATGGATGAACGAAATAGACAGATGCG 1306
QY 4794 TGAGATAGGTCCTCACTGATTAAGCATTTGTAAGTGTACAGCAAGTTTACTATATAT 4853
Db |||||||
QY 1305 TGAGATAGGTCCTCACTGATTAAGCATTTGTAAGTGTACAGCAAGTTTACTATATAT 1246
QY 4854 ACTTTAGATTGATTTAAACTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTT 4913
Db |||||||
QY 1245 ACTTTAGATTGATTTAAACTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTT 1186
QY 4914 TGATAATCTATGACCAAAATCCCTTAACGTGAGTTTTCGTCCACTGAGCGTCAGACCC 4973
Db |||||||
QY 1185 TGATAATCTATGACCAAAATCCCTTAACGTGAGTTTTCGTCCACTGAGCGTCAGACCC 1126
QY 4974 CGTAGAAGATCAAGGATCTCTTGAGATCCCTTTTTCGTGCGGTAAATCTGCTGCTT 5033
Db |||||||
QY 1125 CGTAGAAGATCAAGGATCTCTTGAGATCCCTTTTTCGTGCGGTAAATCTGCTGCTT 1066
QY 5034 GCAACCAAAAAACACCGCTACAGCGGTGCTTTTGTTCGCGATCAAGAGCTACCAAC 5093
Db |||||||
QY 1065 GCAACCAAAAAACACCGCTACAGCGGTGCTTTTGTTCGCGATCAAGAGCTACCAAC 1006
QY 5094 TCTTTTCCGAAGTAACTGGCTTTCAGCAGACGCGAGATACCAAACTACTGTCTTCTAGT 5153
Db |||||||
QY 1005 TCTTTTCCGAAGTAACTGGCTTTCAGCAGACGCGAGATACCAAACTACTGTCTTCTAGT 946
QY 5154 GTAGCCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTGCTCT 5213
Db |||||||
QY 945 GTAGCCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTGCTCT 886
QY 5214 GCTAATCTGTTACAGTGGCTGTCAGTGGCGATGAAGTCGTCTTACCGGTTTGA 5273
Db |||||||
QY 885 GCTAATCTGTTACAGTGGCTGTCAGTGGCGATGAAGTCGTCTTACCGGTTTGA 826
QY 5274 CTCGAAGCATAGTTACCGGATAAGGCGCAGCGTTCGGGCTGAACGGGGGTTCTGTCAC 5333
Db |||||||
QY 825 CTCGAAGCATAGTTACCGGATAAGGCGCAGCGTTCGGGCTGAACGGGGGTTCTGTCAC 766
QY 5334 ACAGCCAGCTTGAAGGAAAGCACTACACCGAATGAGATACCTACAGCTGAGCTATG 5393
Db |||||||
QY 765 ACAGCCAGCTTGAAGGAAAGCACTACACCGAATGAGATACCTACAGCTGAGCTATG 706
QY 5394 AGAAGCGCCACGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGGT 5453
Db |||||||
QY 705 AGAAGCGCCACGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGGT 646
QY 5454 CGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGAGAAACCGCTGATCTTTATAGTCC 5513
Db |||||||
QY 645 CGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGAGAAACCGCTGATCTTTATAGTCC 586
QY 5514 TGTGCGGTTTCCGACCTCTGACTGAGCTGAGCTGATTTTGTGATGCTCTGTCAGGGGGCG 5573
Db |||||||
QY 585 TGTGCGGTTTCCGACCTCTGACTGAGCTGAGCTGATTTTGTGATGCTCTGTCAGGGGGCG 526
QY 5574 GAGCTTATGAAAAACGCGCAGCAACGCGGCTTTTACGGTTCTGCGCTTTTCTGCGCC 5633
Db |||||||
QY 525 GAGCTATCGAAAAACGCGCAGCAACGCGGCTTTTACGGTTCTGCGCTTTTCTGCGCC 466
QY 5634 TTTTGTCTCACAATGTTTCTGCGTTATCCCTGATTTCTGTGGATAACCGTATTACCGC 5693
Db |||||||
QY 465 TTTTGTCTCACAATGTTTCTGCGTTATCCCTGATTTCTGTGGATAACCGTATTACCGC 406
QY 5694 CTTTGTAGTACTGATACCGCTCGCGGAGCGGAAACGAGCGGAGCGAGTCAAGTGAAG 5753
Db |||||||
QY 405 CTTTGTAGTACTGATACCGCTCGCGGAGCGGAAACGAGCGGAGCGAGTCAAGTGAAG 346
QY 5754 CGAGGAAGCGGAAGCGCCCAATACGCAACCGCCCTCTCCCGCGGCTTGGCCGATTCA 5813

Db 345 CGAGAGCGGAAGAGCGCCCAATACGCAACCGCCCTCTCCCGCGGCTTGGCCGATTCA 286
QY 5814 TTAATGCAG 5822
Db |||||||
Db 285 TTAATGCAG 277
RESULT 6
ABT14439/c
ID ABT14439 standard; DNA; 3448 BP.
XX AC ABT14439;
XX 18-FEB-2003 (first entry)
XX HCV envelope protein related vector DNA sequence SEQ ID No 6.
XX Hepatotropic; Hepatitis C Virus; HCV virus; HCV envelope protein; HCV E1;
XX HCV E2; vaccine; Hansenula polymorpha; viral envelope protein;
XX glycosylated; ds.
XX Unidentified.
XX OS
XX WO200286100-A2.
XX 31-OCT-2002.
XX 24-APR-2002; 2002WO-BE000063.
XX 24-APR-2001; 2001EP-00870088.
XX 17-JUL-2001; 2001US-0305604P.
XX (INNO-) INNOGENETICS NV.
XX Bosman A, Depla E, Deschamps G, Sablon E, Samson I;
XX Van Broekhoven A, Haelewyn J;
XX WPI; 2003-093130/08.
XX New Hepatitis C Virus (HCV) virus-like particle formed of an HCV envelope
XX protein or its part, useful for treating or preventing HCV infection.
XX Example 7; Page 158-160; 296pp; English.
XX The invention relates to a Hepatitis C Virus (HCV) virus-like particle
XX formed of an HCV envelope protein or its part, where the cysteines are
XX chemically and reversibly modified. The HCV E1 and/or HCV E2 proteins are
XX useful for the manufacture of a vaccine or medication against HCV
XX infection or for preparing a diagnostic kit. The Hansenula polymorpha is
XX useful for the expression of viral envelope proteins that become
XX glycosylated upon expression in this yeast species. This polynucleotide
XX sequence represents the DNA of a vector relating to the HCV envelope
XX proteins of the invention
XX
SQ Sequence 3448 BP; 861 A; 882 C; 879 G; 823 T; 0 U; 3 Other;
Query Match 46.0%; Score 2680.4; DB 7; Length 3448;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2690; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3294 CCCAACAGTTGCGACGCTGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGC 3353
Db CCCAACAGTTGCGACGCTGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGC 2746
QY 3354 GCGGGGTGTGGTTACGGCGAGCTGACCGCTACATTGCGAGCGCCCTAGCGCCGC 3413
Db GCGGGGTGTGGTTACGGCGAGCTGACCGCTACATTGCGAGCGCCCTAGCGCCGC 2686
QY 3414 TCCCTTCGCTTCTTCCCTTCCCTTTCGCGCAGTTTCGCGCGCTTTCGCCGTCAAGCTCT 3473
Db TCCCTTCGCTTCTTCCCTTCCCTTTCGCGCAGTTTCGCGCGCTTTCGCCGTCAAGCTCT 2626
QY 3474 AATTCGGGGCTCCCTTTAGGGTTCGANTTAGAGCTTTTACGGCACTCGACCGCAAAAA 3533
Db AATTCGGGGCTCCCTTTAGGGTTCGANTTAGAGCTTTTACGGCACTCGACCGCAAAAA 2566
QY 3534 ACTTGATTGGGTGATGGTTACGTAGTGGCCATCGCCCTGTAGAGCGTTCCTCGCCC 3593
Db ACTTGATTGGGTGATGGTTACGTAGTGGCCATCGCCCTGTAGAGCGTTCCTCGCCC 2506
QY 3594 TTTGACGTTGGAGTCCACGTTCTTTAATAGTGAACCTTCTGTTCCAAACTGGAAACAACCT 3653
Db TTTGACGTTGGAGTCCACGTTCTTTAATAGTGAACCTTCTGTTCCAAACTGGAAACAACCT 2446
QY 3654 CAACCCCTATCTCGTCTATTTCTTTTGAATTAAGGGATTTGCGGATTTTCGGCCTATTG 3713
Db CAACCCCTATCTCGTCTATTTCTTTTGAATTAAGGGATTTGCGGATTTTCGGCCTATTG 2386
QY 3714 GTTAAAAAATGAGCTGATTTTAAACAATTTTAAACGGCAATTTTAAACAATATTAAAGTT 3773
Db GTTAAAAAATGAGCTGATTTTAAACAATTTTAAACGGCAATTTTAAACAATATTAAAGTT 2326
QY 3774 TACAATTTCCGCTGATCGGCTATTTCTCTTACGCACTCTGCGGTATTTTCAACCGCA 3833
Db TACAATTTCCGCTGATCGGCTATTTCTCTTACGCACTCTGCGGTATTTTCAACCGCA 2266
QY 3834 TACAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAAT 3893
Db TACAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAAT 2206
QY 3894 ACATTCAAAATATGATTCGCTCATGACACAATACCTGATAATGCTTCAATAATATG 3953
Db ACATTCAAAATATGATTCGCTCATGACACAATACCTGATAATGCTTCAATAATATG 2146
QY 3954 AAAAAAGAGATGATGAGTATTCAAACATTTCCGCTGCGCCCTATTCCCTTTTTCGGC 4013
Db AAAAAAGAGATGATGAGTATTCAAACATTTCCGCTGCGCCCTATTCCCTTTTTCGGC 2086
QY 4014 ATTTTGCCTTCCCTTTTGTGTCACCCAGAAACGCTGGTGAAAGTAAAGATGCTGAAGA 4073
Db ATTTTGCCTTCCCTTTTGTGTCACCCAGAAACGCTGGTGAAAGTAAAGATGCTGAAGA 2026
QY 4074 TCAGTTGGGTGACGAGTGGGTATCATCGAACTGGAATCTCAACAGCGGTAAAGTCCCTGA 4133
Db TCAGTTGGGTGACGAGTGGGTATCATCGAACTGGAATCTCAACAGCGGTAAAGTCCCTGA 1966
QY 4134 GAGTTTTTCGCCCCGAAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGCG 4193
Db GAGTTTTTCGCCCCGAAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGCTCA 1906
QY 4194 CGCGGTATTTATCCGTTATTCAGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTC 4253
Db TACACTATTATCCGTTATTCAGCGCGGCAAGAGCAACTCGGTGCGCGCGGTATTC 1846
QY 4254 TCAGAAATGACTTGGTTCAGTACTCACAGTCAAGAAAGCACTTACGGATGGCATGAC 4313
Db TCAGAAATGACTTGGTTCAGTACTCACAGTCAAGAAAGCACTTACGGATGGCATGAC 1786
QY 4314 AGTAAGAGAAATATSCAGTGTGCTCAATACCATGAGTGATAACACTCGCGCCCACTTACT 4373
Db AGTAAGAGAAATATGCAGTGTGCTCAATACCATGAGTGATAACACTCGCGCCCACTTACT 1726
QY 4374 TCTGACAACGATTCGAGACCGAAGGAGCTAACCGCTTTTTTGGCAACAATGGGGATCA 4433

Db 1725 TCTGACAAAGATCGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAAATGGGGATCA 1666
QY 4434 TGTAACTCGCTTGATCGTTTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGACGAGCG 4493
Db TGTAACTCGCTTGATCGTTTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGACGAGCG 1606
QY 4494 TGAACACGATCGCTGTAGCAATGGCAACAAAGTTTGCAGAACTATTAACTGCGCAACT 4553
Db TGAACACGATCGCTGTAGCAATGGCAACAAAGTTTGCAGAACTATTAACTGCGCAACT 1546
QY 4554 ACTTACTAGCTTCCGGCAACAAATTAATAGACTGATGGAGCGGATTAAGTTGAGG 4613
Db ACTTACTAGCTTCCGGCAACAAATTAATAGACTGATGGAGCGGATTAAGTTGAGG 1486
QY 4614 ACCACTTTCGCGCTCGGCCCTTCCGCTGCTGTTTATTGCTGATAAACTCTGGAGCGG 4673
Db ACCACTTTCGCGCTCGGCCCTTCCGCTGCTGTTTATTGCTGATAAACTCTGGAGCGG 1426
QY 4674 TGAGCGTGGGTCTCGCGGTATCATTTGAGCACTTGGGGCAGATGGTAAAGCCCTCCCGTAT 4733
Db TGAGCGTGGGTCTCGCGGTATCATTTGAGCACTTGGGGCAGATGGTAAAGCCCTCCCGTAT 1366
QY 4734 CGTAGTTATCTACAGACGGGGAGTCAAGCAACTATATGATGAACGAATAGACAGATCGC 4793
Db CGTAGTTATCTACAGACGGGGAGTCAAGCAACTATATGATGAACGAATAGACAGATCGC 1306
QY 4794 TGAGATAGGTGCTCTACTGATTAAGCACTTGGTAACTGTAGCAAGCTTTTACTCATATAT 4853
Db TGAGATAGGTGCTCTACTGATTAAGCACTTGGTAACTGTAGCAAGCTTTTACTCATATAT 1246
QY 4854 ACTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATTCCTTTT 4913
Db ACTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATTCCTTTT 1186
QY 4914 TGAATATCTCATGACCAAAATCCCTTAAACGTTAGTTTTCGTTCACTGAGCGTCAGACCC 4973
Db TGAATATCTCATGACCAAAATCCCTTAAACGTTAGTTTTCGTTCACTGAGCGTCAGACCC 1126
QY 4974 CGTAGAAAAGATCAAAAGGATCTTCTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTT 5033
Db CGNNNAAAAGATCAAAAGGATCTTCTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTT 1066
QY 5034 GCAAAACAAAAACCAACCGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGTACCAAC 5093
Db GCAAAACAAAAACCAACCGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGTACCAAC 1006
QY 5094 TCTTTTTCCGAAGGTAACTGGCTTTCAGCAGCGCAGATACCAATACTCTCTTCTAGT 5153
Db TCTTTTTCCGAAGGTAACTGGCTTTCAGCAGCGCAGATACCAATACTCTCTTCTAGT 946
QY 5154 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 5213
Db GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 886
QY 5214 GCTAATCTCTTACCACTGCTGCTGAGTGGCGATAAGTGTGCTTACCAGGTTTGA 5273
Db GCTAATCTCTTACCACTGCTGCTGAGTGGCGATAAGTGTGCTTACCAGGTTTGA 826
QY 5274 CTCAAGACGATAGTTACCGGATTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTCAC 5333
Db CTCAAGACGATAGTTACCGGATTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTCAC 766
QY 5334 ACAGCCGAGCTTGGAGCAACGACTTACCGCAACTGAGATACCTACAGCGTGAAGTATG 5393
Db ACAGCCGAGCTTGGAGCAACGACTTACCGCAACTGAGATACCTACAGCGTGAAGTATG 706
QY 5394 AGAAAGCGCACTTCCCGAAAGGAGAAAGCGGACAGGTATCCGTTAGCGGACAGGT 5453
Db AGAAAGCGCACTTCCCGAAAGGAGAAAGCGGACAGGTATCCGTTAGCGGACAGGT 646
QY 5454 CGGACAGGAGCGGACAGGAGGCTTCCAGGGGAAACGCTGATCTTTTATCTATCTCC 5513

Db 645 CGGAACAGGAGGAGGACGAGAGCTTCCAGGGGGAAACGCCGTGATCTTTATAGTCC 586
QY 5514 TGTCGGGTTTCGCCACCTCTCACTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCG 5573
Db 585 TGTGGGGTTTCGCCACCTCTCACTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCG 526
QY 5574 GAGCCTATGGAAGAAACGCCAGCAACGCCGCGCTTTTACGGTTCTTGCGCTTTTGTGCGCC 5633
Db 525 GAGCCTATGGAAGAAACGCCAGCAACGCCGCGCTTTTACGGTTCTTGCGCTTTTGTGCGCC 466
QY 5634 TTTTGTCTACATGTTCTTCTGCTTATCCCTGATCTGTGATACCGGTATTAACGC 5693
Db 465 TTTTGTCTACATGTTCTTCTGCTTATCCCTGATCTGTGATACCGGTATTAACGC 406
QY 5694 CTTTGTGAGTGAAGTATGCTGCGGAGCGGAGCGGAGCGGAGCGGAGTCACTGAG 5753
Db 405 CTTTGTGAGTGAAGTATGCTGCGGAGCGGAGCGGAGCGGAGCGGAGTCACTGAG 346
QY 5754 CGAGGAAGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGTCACTGAG 5813
Db 345 CGAGGAAGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGTCACTGAG 286
QY 5814 TTAATGCAG 5822
Db 285 TTAATGCAG 277

RESULT 7

AA29905/C
ID AA29905 standard; DNA; 3018 BP.
AC
AC
AX29905;
XX
XX
DT 06-JUL-1999 (first entry)
XX
XX
DE Plasmid pGEM (RTM) -T Easy Vector.
XX
XX
KW Oligonucleotide; hybridisation; amidated polypeptide; hormone; primer;
KW amplification; rat; brain; cholecystokinin; CCK; amidation; hormone;
KW neurohormone; physiological role; plasmid; ss.
XX
OS Synthetic.
XX
XX
XX WO9910361-A1.
XX
XX
XX 04-MAR-1999.
XX
XX 07-AUG-1998; 98WO-FR001767.
XX
XX 26-AUG-1997; 97FR-00010643.
XX
XX (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
XX
XX Martinez J, Goze C;
XX
XX WPI; 1999-204645/17.
XX
XX
PT Oligonucleotides that hybridize to mRNA encoding precursors of amidated
PT hormones - useful for isolating new hormones.
XX
XX
XX Disclosure; Page 19-21; 27pp; French.
XX
XX The invention relates to single-stranded oligonucleotides of 9-42
XX nucleotides that hybridize, under stringent or non-stringent conditions,
XX with mRNA encoding precursors of amidated polypeptide hormones. This
XX sequence represents the plasmid pGEM (RTM)-T Easy vector used to subclone
XX fragments of amidated polypeptide prohormone coding sequences. The
XX oligonucleotides are used to identify new amidated polypeptide hormones
XX by hybridisation to cDNA encoding their precursors. cDNA encoding the
XX hormones, particularly neurohormones, can be expressed in microorganisms
XX and used therapeutically or to study their physiological roles
XX
XX Sequence 3018 BP; 774 A; 747 C; 767 G; 730 T; 0 U; 0 Other;

Query Match 46.0%; Score 2675.4; DB 2; Length 3018;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2676; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3146 TATAGTGAAGTCTGATTAACAATTTCACTGCGCGCTGTTTTACAAAGCTGCGTGGGAAAC 3205
Db 3018 TATAGTGAAGTCTGATTAACAATTTCACTGCGCGCTGTTTTACAAAGCTGCGTGGGAAAC 2959
QY 3206 CTTGGCGTTACCCAACTTAATCGCTTTCAGCACATCCCCCTTTTCGCCAGCTGGCGTAAT 3265
Db 2958 CTTGGCGTTACCCAACTTAATCGCTTTCAGCACATCCCCCTTTTCGCCAGCTGGCGTAAT 2899
QY 3266 AGCGAAGAGGCGCGCACCGATCGCGCTTCCCAACAGTTGCGCAGCTGAAATGGCGAATGG 3325
Db 2998 AGCGAAGAGGCGCGCACCGATCGCGCTTCCCAACAGTTGCGCAGCTGAAATGGCGAATGG 2839
QY 3326 ACGCCGCTGTAGCGGGCGCATTAAGCGCGCGGGGTGTGCTGTTACGCGCAGCGTGACCG 3385
Db 2938 ACGCCGCTGTAGCGGGCGCATTAAGCGCGGGGTGTGCTGTTACGCGCAGCGTGACCG 2779
QY 3386 CTACACTTGCAGCGCGCTAGCGCGCGCTCCTTTTCGCTTTCCTTCCTTCCTTCGCGCA 3445
Db 2778 CTACACTTGCAGCGCGCTAGCGCGCGCTCCTTTTCGCTTTCCTTCCTTCCTTCGCGCA 2719
QY 3446 CGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGAATTA 3505
Db 2718 CGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGGAATTA 2659
QY 3506 GAGCTTTACGGCAGCTCGACCGCAAAACCTTGATTTGGGTGATGGTTCACTAGTGGCG 3565
Db 2658 GAGCTTTACGGCAGCTCGACCGCAAAACCTTGATTTGGGTGATGGTTCACTAGTGGCG 2599
QY 3566 CATCGCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTG 3625
Db 2598 CATCGCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTG 2539
QY 3626 GACTCTTGTTCGCAACCTGGAACACACTCAACCTATCTCGGTCTATTCCTTTGATTTAT 3685
Db 2538 GACTCTTGTTCGCAACCTGGAACACACTCAACCTATCTCGGTCTATTCCTTTGATTTAT 2479
QY 3686 AAGGGATTTTGGCGATTTTCGCCCTATTGGTTTAAATAATGAGCTGATTTAAACAAATATTTA 3745
Db 2478 AAGGGATTTTGGCGATTTTCGCCCTATTGGTTTAAATAATGAGCTGATTTAAACAAATATTTA 2419
QY 3746 ACGGAAATTTTAAACAAATATTAACGTTTACAATTTTCGCCCTGATTCGGTATTTTCTCCT 3805
Db 2418 ACGGAAATTTTAAACAAATATTAACGTTTACAATTTTCGCCCTGATTCGGTATTTTCTCCT 2359
QY 3806 ACGCATCTGCGGTATTTTCACCGCATACAGGTGGGACATTTTCGGGGAAATGTCGCG 3865
Db 2358 ACGCATCTGCGGTATTTTCACCGCATACAGGTGGGACATTTTCGGGGAAATGTCGCGCG 2299
QY 3866 GAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATATCCGCTCATGAGACAAT 3925
Db 2298 GAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATATCCGCTCATGAGACAAT 2239
QY 3926 AACCTGATAAATGCTTCAATAATTTGAAAAAGGAGATGATGAGTATTTCAACATTTTC 3985
Db 2238 AACCTGATAAATGCTTCAATAATTTGAAAAAGGAGATGATGAGTATTTCAACATTTTC 2179
QY 3986 GTGTGCGGCTTATTCCTTTTTCGCCGATTTTCGCCCTTTCCTTCCTTCCTTCCTCACCGAAA 4045
Db 2178 GTGTGCGGCTTATTCCTTTTTCGCCGATTTTCGCCCTTTCCTTCCTTCCTTCCTCACCGAAA 2119
QY 4046 CGCTGGTGAAGTAAAGATGCTGAAAGTCAAGTTCAGTTGGGTGACGAGTGGGTTACATCGAAC 4105
Db 2118 CGCTGGTGAAGTAAAGATGCTGAAAGTCAAGTTCAGTTGGGTGACGAGTGGGTTACATCGAAC 2059
QY 4106 TGGATCTCAAACAGCGGTAAGATCCTTGAGAGTTCCTTCGCCCGGAGAACGTTTTCCTCAATGA 4165
Db 2058 TGGATCTCAAACAGCGGTAAGATCCTTGAGAGTTCCTTCGCCCGGAGAACGTTTTCCTCAATGA 1999

```
QY 4166 TGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGAACGCCGGCAAG 4225
Db 1998 TGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGAACGCCGGCAAG 1939
QY 4226 AGCAACTCGGTGCGCGGATACACTATTCTCAGAAATGACTTGGTTGAGTACTCAGCAGTCA 4285
Db 1938 AGCAACTCGGTGCGCGGATACACTATTCTCAGAAATGACTTGGTTGAGTACTCAGCAGTCA 1879
QY 4286 CAGAAAGCATCTTACGGATGGGATGACAGTAGAGAAATATCAGTGTCCCATACCA 4345
Db 1878 CAGAAAGCATCTTACGGATGGGATGACAGTAGAGAAATATCAGTGTCCCATACCA 1819
QY 4346 TGAGTGATAACTCTGCGGCCAACTTACTCTGCAACGATCGGAGGACCGAAGAGCTAA 4405
Db 1818 TGAGTGATAACTCTGCGGCCAACTTACTCTGCAACGATCGGAGGACCGAAGAGCTAA 1759
QY 4406 CCGTTTTTTTGGCAACAATCGGGGATCATGTAACTCGCCTTGATCGTTGGAAACCGGAGC 4465
Db 1758 CCGTTTTTTTGGCAACAATCGGGGATCATGTAACTCGCCTTGATCGTTGGAAACCGGAGC 1699
QY 4466 TGAATGAAGCCATACCAAAACGACGAGCGTGACACCGATGCCCTGTAGCAATGGCAACAA 4525
Db 1698 TGAATGAAGCCATACCAAAACGACGAGCGTGACACCGATGCCCTGTAGCAATGGCAACAA 1639
QY 4526 CGTTGGCAAACTATTAACTGGGAACTACTTCTAGCTTCCCGCAACAATAATAG 4585
Db 1638 CGTTGGCAAACTATTAACTGGGAACTACTTCTAGCTTCCCGCAACAATAATAG 1579
QY 4586 ACTGGATGGAGGCGGATAAAGTTTCAGGACCACTTCTGGCGTCGGCCCTTCCGGCTGGCT 4645
Db 1578 ACTGGATGGAGGCGGATAAAGTTTCAGGACCACTTCTGGCGTCGGCCCTTCCGGCTGGCT 1519
QY 4646 GGTATTATGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCAC 4705
Db 1518 GGTATTATGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCAC 1459
QY 4706 TGGGGCCAGATGTAAGCCCTCCGCTATCGTATCTAGTATCTACAGACGGGAGTCAGGCAA 4765
Db 1458 TGGGGCCAGATGTAAGCCCTCCGCTATCGTATCTAGTATCTACAGACGGGAGTCAGGCAA 1399
QY 4766 CTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGGCTCACTGATTAAGCATTTGGT 4825
Db 1398 CTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGGCTCACTGATTAAGCATTTGGT 1339
QY 4826 AACTGTGAGACCAAGTTTACTCATATATACATTTAGATTGATTTAAACTTCAATTTTAAAT 4885
Db 1338 AACTGTGAGACCAAGTTTACTCATATATACATTTAGATTGATTTAAACTTCAATTTTAAAT 1279
QY 4886 TTAAAGGATCTAGGTGAAGATCCCTTTTGTATACTCATGACCAAAATCCCTTAAACGTG 4945
Db 1278 TTAAAGGATCTAGGTGAAGATCCCTTTTGTATACTCATGACCAAAATCCCTTAAACGTG 1219
QY 4946 AGTTTTGTTCCACTGAGCGTCAGACCCCGTAGAAAGATCAAGGATCTCTTGTAGATC 5005
Db 1218 AGTTTTGTTCCACTGAGCGTCAGACCCCGTAGAAAGATCAAGGATCTCTTGTAGATC 1159
QY 5006 CTTTTTTTCTCGCGGTAACTCGCTGTGCTTGCAAAACAAAAACCAACCGCTACACGCGTGG 5065
Db 1158 CTTTTTTTCTCGCGGTAACTCGCTGTGCTTGCAAAACAAAAACCAACCGCTACACGCGTGG 1099
QY 5066 TTTGTTTGGCGGATCAAGAGTACCAACTCTTTTTCGAAAGGTAACTGGCTTCAGAGAG 5125
Db 1098 TTTGTTTGGCGGATCAAGAGTACCAACTCTTTTTCGAAAGGTAACTGGCTTCAGAGAG 1039
QY 5126 CGCAGATACCAAACTACTGCTCTTAGGTAGCGTAGTTAGGCCAACCACTTCAAGAACT 5185
Db 1038 CGCAGATACCAAACTACTGCTCTTAGGTAGCGTAGTTAGGCCAACCACTTCAAGAACT 979
QY 5186 CTGTAGCACCGGCTACATACCTCGCTCTGTCTTAATCTGTTTACCAGTGGCTGCCAGTG 5245
Db 978 CTGTAGCACCGGCTACATACCTCGCTCTGTCTTAATCTGTTTACCAGTGGCTGCCAGTG 919
QY 5246 GCGATAAGTCTGTCTTACCAGGTTGGACTCAAGACGATAGTTTACCGGATAAGGCGCAGC 5305
```

```
Db 918 GCATTAAGTCTGTCTTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCAGC 859
QY 5306 GGTCCGGCTGAACCGGGGTTCTGTGCACACAGCCAGCTTGGAGCGAAACGACCTACACCG 5365
Db 858 GGTCCGGCTGAACCGGGGTTCTGTGCACACAGCCAGCTTGGAGCGAAACGACCTACACCG 799
QY 5366 AACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCACGCTTCCCGAAGGGAAGG 5425
Db 798 AACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCACGCTTCCCGAAGGGAAGG 739
QY 5426 CGACAGGATATCCGTTAAGCGGAGGTGGAACAGGAGCGCACGAGGAGTTCAG 5485
Db 738 CGACAGGATATCCGTTAAGCGGAGGTGGAACAGGAGCGCACGAGGAGTTCAG 679
QY 5486 GGGGAAACGCTGATCTTTATAGTCTCTGTCGGGTTTCGCCACTCTGACTTGAGGCTC 5545
Db 678 GGGGAAACGCTGATCTTTATAGTCTCTGTCGGGTTTCGCCACTCTGACTTGAGGCTC 619
QY 5546 GATTTTGTGATGCTCGTCAAGGGGCGGAGCCTATGAAAAACGCGCAACCGCGCCT 5605
Db 618 GATTTTGTGATGCTCGTCAAGGGGCGGAGCCTATGAAAAACGCGCAACCGCGCCT 559
QY 5606 TTTTACGGTTCTGGCCCTTTTGTGSCCTTTTGTGTCATGTTCTTCTGCGTTATCCC 5665
Db 558 TTTTACGGTTCTGGCCCTTTTGTGSCCTTTTGTGTCATGTTCTTCTGCGTTATCCC 499
QY 5666 CTGATTCTGTGGATTAACCGTATTACCGCTTTTGAGTGAGTGTATACCGCTCGCGCAGCC 5725
Db 498 CTGATTCTGTGGATTAACCGTATTACCGCTTTTGAGTGAGTGTATACCGCTCGCGCAGCC 439
QY 5726 GAACGACCGGAGCGCAGCGAGTCACTGAGCGAGGAGCGAAGCGCCCAATACGCAAC 5785
Db 438 GAACGACCGGAGCGCAGCGAGTCACTGAGCGAGGAGCGAAGCGCCCAATACGCAAC 379
QY 5786 CGCCTCTCCCGCGGCTTGGCCGATTCATTAAATGCAG 5822
Db 378 CGCCTCTCCCGCGGCTTGGCCGATTCATTAAATGCAG 342

RESULT 8
AAD0980/c
ID AAD0980 standard; DNA; 5919 BP.
XX
AC AAD0980;
XX
DT 12-SEP-2001 (first entry)
XX
pHSP-GUS construct for transfection of pacific oysters.
XX
Fruitfly; fertility; reproduction; gametogenesis; microinjection; GUS;
KW glucuronidase; infection; plasmid pHSP-GUS; HSP; heat shock promoter;
KW embryogenesis; ds.
XX
OS Drosophila melanogaster.
OS Unidentified.
OS Chimeric.
XX
PN WO200148224-A1.
XX
PD 05-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-AU001596.
XX
PR 24-DEC-1999; 99AU-00004884.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Thresher R, Hinds L, Hardy C, Whyard S, Vignarajan S, Grewe PW;
PI Patil J;
XX
DR WPI; 2001-425672/45.
XX
```


PT Novel construct for preventing embryogenesis in animals comprises native
PT promoter, blocking DNA which abrogates function of crucial gene and
PT genetic switch to regulate expression/repression of blocker/gene
PT knockout.
XX
PS Example 8; Page 196-198; 24lpp; English.
XX
CC The invention relates to a construct which allows animals to be bred in
CC captivity but renders them infertile in the wild by allowing reversible
CC control over fertility and reproduction. The construct comprises a native
CC promoter, a blocking DNA sequence contoured for and designed to abrogate
CC a crucial gene's function or to cause its mis-expression, and a genetic
CC switch to regulate controlled expression/repression of the blocker/gene
CC knockout. The construct is useful for preventing embryogenesis or
CC gametogenesis in animals by stably transforming an animal cell with the
CC construct by microinjection, transfection or infection, where the
CC construct stably integrates into the genome by homologous recombination,
CC and implanting the cell into a host organism, where a whole animal
CC develops from the implanted cell. The present DNA sequence is plasmid
CC construct pHSP-GUS construct used for transfection of Pacific oysters.
CC The plasmid contains glucuronidase (GUS) gene under the control of
CC Drosophila heat shock promoter (dHSP)
XX
SQ Sequence 5919 BP; 1504 A; 1474 C; 1414 G; 1527 T; 0 U; 0 Other;
Query Match 46.0%; Score 2675.4; DB 4; Length 5919;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2676; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3146 TATAGTCAGTCGTATTAACTACTCGCGCTGCTTTTAAACGTCGTACTGGGAAAC 3205
DB 5919 TATAGTCAGTCGTATTAACTACTCGCGCTGCTTTTAAACGTCGTACTGGGAAAC 5860
QY 3206 CCTGGCGTTACCCAACTTAATCGCTTTGCAGCACATCCCGCTTCGCCAGCTGCGTAAT 3265
DB 5859 CCTGGCGTTACCCAACTTAATCGCTTTGCAGCACATCCCGCTTCGCCAGCTGCGTAAT 5800
QY 3266 AGCGAAGAGCGCCGACCGATCGCCCTTCCAAACAGTTGCGCAGCCGTGAATGGCAATGG 3325
DB 5799 AGCGAAGAGCGCCGACCGATCGCCCTTCCAAACAGTTGCGCAGCCGTGAATGGCAATGG 5740
QY 3326 ACGCGCCCTGTAGCGGCGATTAGCGCGCGGTGTGGTTACCGGAGCGGTGACCG 3385
DB 5739 ACGCGCCCTGTAGCGGCGATTAGCGCGCGGTGTGGTTACCGGAGCGGTGACCG 5680
QY 3386 CTACACTTGCAGCGCCCTAGCGCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTCGCGCA 3445
DB 5679 CTACACTTGCAGCGCCCTAGCGCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTCGCGCA 5620
QY 3446 CGTTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTA 3505
DB 5619 CGTTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTA 5560
QY 3506 GAGCTTTAGCGCAGCTCGACCGCAAAACCTTGATTTGGGTGATGTTTCAGTAGTGGC 3565
DB 5559 GAGCTTTAGCGCAGCTCGACCGCAAAACCTTGATTTGGGTGATGTTTCAGTAGTGGC 5500
QY 3566 CATCGCCCTGATAGACGGTTTTCGCGCTTTGAGCGTTGGAGTCCACGTTCTTTAATAGTG 3625
DB 5499 CATCGCCCTGATAGACGGTTTTCGCGCTTTGAGCGTTGGAGTCCACGTTCTTTAATAGTG 5440
QY 3626 GACTCTGTTCCAACTCGGAACAACACTCAACCCCTATCTCGGCTATCTCTTTGATTAT 3685
DB 5439 GACTCTGTTCCAACTCGGAACAACACTCAACCCCTATCTCGGCTATCTCTTTGATTAT 5380
QY 3686 AAGGATTTTCGGATTTTCGGCTATTGTTTAAATAATGAGCTGATTTTAAACAATATTTA 3745
DB 5379 AAGGATTTTCGGATTTTCGGCTATTGTTTAAATAATGAGCTGATTTTAAACAATATTTA 5320
QY 3746 ACGGAATTTTAAACAAATATTAAAGTTTACAATTTGCGCTGATCGCGTATTTTCTCCTT 3805
DB 5319 ACGGAATTTTAAACAAATATTAAAGTTTACAATTTGCGCTGATCGCGTATTTTCTCCTT 5260

QY 3806 ACCCATCTGCGGTATTTTCCACCGCATACAGTGGCAGCTTTTCGGGGAAATGTGCGG 3865
DB 5259 ACCCATCTGCGGTATTTTCCACCGCATACAGTGGCAGCTTTTCGGGGAAATGTGCGG 5200
QY 3866 GAACCCCTATTTGTTTATTTTCTTAATAATCAATTCATATATGTATCCGCTCATGACAAT 3925
DB 5199 GAACCCCTATTTGTTTATTTTCTTAATAATCAATTCATATATGTATCCGCTCATGACAAT 5140
QY 3926 AACCTGATTAATGCTTCAATAATATGAAAAAGGAGATGATGATTAATCAATTTCC 3985
DB 5139 AACCTGATTAATGCTTCAATAATATGAAAAAGGAGATGATGATTAATCAATTTCC 5080
QY 3986 GTGTCGCCCTTATTTCCCTTTTTCGGGCAATTTTGCCTTCTGTTTTCCTCACCAGAAA 4045
DB 5079 GTGTCGCCCTTATTTCCCTTTTTCGGGCAATTTTGCCTTCTGTTTTCCTCACCAGAAA 5020
QY 4046 CGCTGTGTAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGATGGGTACATCGAAC 4105
DB 5019 CGCTGTGTAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGATGGGTACATCGAAC 4960
QY 4106 TGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTTCATGA 4155
DB 4959 TGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTTCATGA 4900
QY 4166 TGAGCCTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAG 4225
DB 4899 TGAGCCTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAG 4840
QY 4226 AGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACAGTCA 4285
DB 4839 AGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACAGTCA 4780
QY 4286 CAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGSCAGTGTGTCATTAACCA 4345
DB 4779 CAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGSCAGTGTGTCATTAACCA 4720
QY 4346 TGAGTGATAACACTTGGCGCAACTTACTCTGACAAAGATCGGAGGACCGAAGAGCTAA 4405
DB 4719 TGAGTGATAACACTTGGCGCAACTTACTCTGACAAAGATCGGAGGACCGAAGAGCTAA 4660
QY 4406 CCGCTTTTTCGACAAACATGGGGGATCATGTAACTCGCTTGTGATGCTTGGGAAACCGGAGC 4465
DB 4659 CCGCTTTTTCGACAAACATGGGGGATCATGTAACTCGCTTGTGATGCTTGGGAAACCGGAGC 4600
QY 4466 TGAATGAAGCATATCCAAAACGAGCGGTGACACCAAGTCCCTGTAGCAATGCAACAA 4525
DB 4599 TGAATGAAGCATATCCAAAACGAGCGGTGACACCAAGTCCCTGTAGCAATGCAACAA 4540
QY 4526 CGTTTCGCAAACTATTAACTGGCGAACTTACTCTAGCTTCCCGGCAACAAATTAATAG 4585
DB 4539 CGTTTCGCAAACTATTAACTGGCGAACTTACTCTAGCTTCCCGGCAACAAATTAATAG 4480
QY 4586 ACTGGATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGGCCCTTCGCGCTGGCT 4645
DB 4479 ACTGGATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGGCCCTTCGCGCTGGCT 4420
QY 4646 GGTATTATGCTGATAAATCTGGAGCCCGGTGAGCGGTGCTGCGGGTATCATTTGAGCAC 4705
DB 4419 GGTATTATGCTGATAAATCTGGAGCCCGGTGAGCGGTGCTGCGGGTATCATTTGAGCAC 4360
QY 4706 TGGGGCCAGATGTAAGCCCTCCGCTATCGTAGTTTCTACACGACGGGAGTCAAGGCAA 4765
DB 4359 TGGGGCCAGATGTAAGCCCTCCGCTATCGTAGTTTCTACACGACGGGAGTCAAGGCAA 4300
QY 4766 CTATGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCTCATGATTAAGCATTTGGT 4825
DB 4299 CTATGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCTCATGATTAAGCATTTGGT 4240
QY 4826 AACTGTGAGCAAGATTTTACTCATATATATCTTTAGATGATTTTAAACCTCATTTTAAAT 4885
DB 4239 AACTGTGAGCAAGATTTTACTCATATATATCTTTAGATGATTTTAAACCTCATTTTAAAT 4180
QY 4886 TTAAAGGATCTAGGTGAAGATCCTTTTGTATATCTCATGACCAAAATCCCTTTAAACGTG 4945

Db 2748 GGCGGTTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCAGCGCCTAGCGCCGCG 2689
QY 3414 TCCCTTCCCTTCTTCCCTTCTTCCCTTCTGCGCAGCTTCCGCGCTTCCCGTCAAGCTCT 3473
Db 2698 TCCCTTCCCTTCTTCCCTTCTTCCCTTCTGCGCAGCTTCCGCGCTTCCCGTCAAGCTCT 2629
QY 3474 AAATCGGGGGTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAA 3533
Db 2628 AAAATCGGGGGTCCCTTTAGGGTTCCGATTTAGTGGTTTACGGCACCTCGACCGCAAAA 2569
QY 3534 ACTTGATTTGGGTGATGTTTCACTGATGAGGTCATCGCCCTGATAGAGGTTTTTCGGCC 3593
Db 2568 ACTTGATTTAGGTGATGTTTCACTGATGAGGTCATCGCCCTGATAGAGGTTTTTCGGCC 2509
QY 3594 TTTGACGTTGGAGTCCAGCTTCTTTAAATAGTGGACTCTGTTCCAAAATGGAACAACACT 3653
Db 2508 TTTGACGTTGGAGTCCAGCTTCTTTAAATAGTGGACTCTGTTCCAAAATGGAACAACACT 2449
QY 3654 CAACCTATCTCGGTCTATTTCTTTGATTTATAAGGGATTTTCCGATTTCCGCGATTTG 3713
Db 2448 CAACCTATCTCGGTCTATTTCTTTGATTTATAAGGGATTTTCCGATTTTCCGCGATTTG 2389
QY 3714 GTTAAAAAATGAGCTGATTTTAAACAAATATTTAAACGCGAATTTTAAACAAAATATTAACGCT 3773
Db 2388 GTTAAAAAATGAGCTGATTTTAAACAAATATTTAAACGCGAATTTTAAACAAAATATTAACGCT 2329
QY 3774 TACAAATTTCCGCTGATGCGGTATTTTCTCTTACGATCTGTGCGGTATTTTCAACCGCA 3833
Db 2328 TACAAATTT - CCTGATGCGGTATTTTCTCTTACGATCTGTGCGGTATTTTCAACCGCA 2271
QY 3834 TACAGTGGCACTTTTCCGGGAAATGTCGGGAACTTTCGCGGAACTTTCGCGGTATTTTCTAAAT 3893
Db 2270 T - CAGTGGCACTTTTCCGGGAAATGTCGGGAACTTTCGCGGAACTTTCGCGGTATTTTCTAAAT 2212
QY 3894 ACATTCAAATATGATTCGCTCATGAGACAATAACCTCTGATAAATGCTTCAATATATG 3953
Db 2211 ACATTCAAATATGATTCGCTCATGAGACAATAACCTCTGATAAATGCTTCAATATATG 2152
QY 3954 AAAAGGAGATGATGATTAACAATTTCCGTCGCGCTTATTCCTTTTTCGGC 4013
Db 2151 AAAAGGAGATGATGATTAACAATTTCCGTCGCGCTTATTCCTTTTTCGGC 2092
QY 4014 ATTTTGCCTTCTGTTTGTCTACCCAGAAAGCTGTGAAAGTAAAGATGCTGAGA 4073
Db 2091 ATTTTGCCTTCTGTTTGTCTACCCAGAAAGCTGTGAAAGTAAAGATGCTGAGA 2032
QY 4074 TCAGTTGGTGCACGAGTGGTTACATCGAACTGGATCTCAACAGCGTAAAGTCTTGA 4133
Db 2031 TCAGTTGGTGCACGAGTGGTTACATCGAACTGGATCTCAACAGCGTAAAGTCTTGA 1972
QY 4134 GAGTTTTCGCGCGAGAACGTTTTCOAATGATGAGCACTTTTAAAGTCTGCTATG 4193
Db 1971 GAGTTTTCGCGCGAGAACGTTTTCOAATGATGAGCACTTTTAAAGTCTGCTATG 1912
QY 4194 CGCGTATTTATCCGTTATGACGCGGCAAGACAACTCGTTCGCGCAACACTATTC 4253
Db 1911 CGCGTATTTATCCGTTATGACGCGGCAAGACAACTCGTTCGCGCAACACTATTC 1852
QY 4254 TCAGAATGACTTGGTTGAGTACTCACCACTCACGAAAGCATCTTACGGATGGCATGAC 4313
Db 1851 TCAGAATGACTTGGTTGAGTACTCACCACTCACGAAAGCATCTTACGGATGGCATGAC 1792
QY 4314 AGTAAGAAATATGAGTGTGCTGATTAACATGATGATTAACACTTGGCGCAACTTACT 4373
Db 1791 AGTAAGAAATATGAGTGTGCTGATTAACATGATGATTAACACTTGGCGCAACTTACT 1732
QY 4374 TCTGACACGATCGGAGACGAGGAGCTAACCGCTTTTTCGACAACTGCGGGATCA 4433
Db 1731 TCTGACACGATCGGAGACGAGGAGCTAACCGCTTTTTCGACAACTGCGGGATCA 1672
QY 4434 TGTAACCTCGCTTGTATTCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACAGCAGCG 4493

Db 1671 TGTAACCTCGCTTGTATTCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 1612
QY 4494 TGACACACGATGCTGTAGCAATGGCAACAAACGTTGGCGAAACTATTAACTGGCGAACT 4553
Db 1611 TGACACACGATGCTGTAGCAATGGCAACAAACGTTGGCGAAACTATTAACTGGCGAACT 1552
QY 4554 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGAG 4613
Db 1551 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGAG 1492
QY 4614 ACCACTTCTGCGCTCGGCCCTTCCGCTCGGCTGGTTTATTTGCTGATAAATCTGGAGCGCG 4673
Db 1491 ACCACTTCTGCGCTCGGCCCTTCCGCTCGGCTGGTTTATTTGCTGATAAATCTGGAGCGCG 1432
QY 4674 TGAGGCTGGTCTCGCGGTATCATTTGACGACTGGGGCCAGATGTAGACCCCTCCGCTAT 4733
Db 1431 TGAGGCTGGTCTCGCGGTATCATTTGACGACTGGGGCCAGATGTAGACCCCTCCGCTAT 1372
QY 4734 CGTAGTTATCTACAGCGGGGAGTCAAGCACTATTTGATGAACGAATAGACAGATCGC 4793
Db 1371 CGTAGTTATCTACAGCGGGGAGTCAAGCACTATTTGATGAACGAATAGACAGATCGC 1312
QY 4794 TGAGTAGGTCCTTCACTGATTAAGCACTTGTAACTGTCAAGCAAACTTACTCATATAT 4853
Db 1311 TGAGTAGGTCCTTCACTGATTAAGCACTTGTAACTGTCAAGCAAACTTACTCATATAT 1252
QY 4854 ACTTTAGATGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 4913
Db 1251 ACTTTAGATGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 1192
QY 4914 TGATAATCTCATGACCAAAATCCCTTAACGCTGAGTTTTCGTCCTCACTGAGCGTCAAGCC 4973
Db 1191 TGATAATCTCATGACCAAAATCCCTTAACGCTGAGTTTTCGTCCTCACTGAGCGTCAAGCC 1132
QY 4974 CGTAGAAAAGATCAAGGATCTTCTTGAGATCTTTCGTCGCGTAACTCGCTGCTT 5033
Db 1131 CGTAGAAAAGATCAAGGATCTTCTTGAGATCTTTCGTCGCGTAACTCGCTGCTT 1072
QY 5034 GCAACAAAAAACAACCGCTACAGCGGTGGTTTGGTTGCGGATCAAGAGTCAAC 5093
Db 1071 GCAACAAAAAACAACCGCTACAGCGGTGGTTTGGTTGCGGATCAAGAGTCAAC 1012
QY 5094 TCTTTTTCGAGGATTAAGTCTTACAGCGCGGAGTCAAGATCTGCTCTCTAGT 5153
Db 1011 TCTTTTTCGAGGATTAAGTCTTACAGCGCGGAGTCAAGATCTGCTCTCTAGT 952
QY 5154 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT 5213
Db 951 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT 892
QY 5214 GCTAATCTCTGTTACAGTGGTGTCTGCGAGTGGGATAGTCTGTTTACCGGTTGGA 5273
Db 891 GCTAATCTCTGTTACAGTGGTGTCTGCGAGTGGGATAGTCTGTTTACCGGTTGGA 832
QY 5274 CTCAGACGATAGTTACCGGATAGGCGCGCTCGGCTGAAAGCGGGGTTGCGCAC 5333
Db 831 CTCAGACGATAGTTACCGGATAGGCGCGCTCGGCTGAAAGCGGGGTTGCGCAC 772
QY 5334 ACAGCCAGCTTTGAGCGAAACGACTTACACCGAACTGAGATACCTACAGCTGAGCTATG 5393
Db 771 ACAGCCAGCTTTGAGCGAAACGACTTACACCGAACTGAGATACCTACAGCTGAGCTATG 712
QY 5394 AGAAGCGCACTTCCGAAAGGAGAAAGCGGACAGGATATCCGTTAAGCGGAGG 5453
Db 711 AGAAGCGCACTTCCGAAAGGAGAAAGCGGACAGGATATCCGTTAAGCGGAGG 652
QY 5454 CGGACAGGAGAGCGCAGGAGGAGCTTCCAGGGGAAAAGCGCTGATCTTTATAGTCC 5513
Db 651 CGGACAGGAGAGCGCAGGAGGAGCTTCCAGGGGAAAAGCGCTGATCTTTATAGTCC 592
QY 5514 TGTCCGGTTTCCGCACTCTGACTTGTAGCGTTCGATTTTGTGATGCTCGTCAGGGGGCG 5573
Db 591 TGTCCGGTTTCCGCACTCTGACTTGTAGCGTTCGATTTTGTGATGCTCGTCAGGGGGCG 532

4014 ATTTTGGCTTCTCTGTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGTGTCTGAAGA 4073
Db |||||
2091 ATTTTGGCTTCTCTGTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGTGTCTGAAGA 2032
Qy |||||
4074 TCAGTTGGGTGCACAGTGGGTATACATCGAACTGGATCTCAACAGCGGTAAAGTCTCTTGA 4133
Db |||||
2031 TCAGTTGGGTGCACAGTGGGTATACATCGAACTGGATCTCAACAGCGGTAAAGTCTCTTGA 1972
Qy |||||
4134 GAGTTTGGCCCGAAGACGTTTTCATGATGAGCACTTTTAAAGTCTCTGCTATGTGG 4193
Db |||||
1971 GAGTTTGGCCCGAAGACGTTTTCATGATGAGCACTTTTAAAGTCTCTGCTATGTGG 1912
Qy |||||
4194 GCGGTAATATCCGTAATGAGCGGGGCRAGAGCACTCGTGGCCGCATACACTATTTC 4253
Db |||||
1911 GCGGTAATATCCGTAATGAGCGGGGCRAGAGCACTCGTGGCCGCATACACTATTTC 1852
Qy |||||
4254 TCAGATGACTTGGTTGAGTACTCACAGTCAACAGAAAGCATCTTACGATGGCATGAC 4313
Db |||||
1851 TCAGATGACTTGGTTGAGTACTCACAGTCAACAGAAAGCATCTTACGATGGCATGAC 1792
Qy |||||
4314 AGTAAGAGAAATATGAGTGTGGTGCATTAACATGAGTGATTAACACTGGGGCCAACTTACT 4373
Db |||||
1791 AGTAAGAGAAATATGAGTGTGGTGCATTAACATGAGTGATTAACACTGGGGCCAACTTACT 1732
Qy |||||
4374 TCTGACAAACGATCGAGGACCGAAGGAGCTAACCGCTTTTTCACAACTGGGGGATCA 4433
Db |||||
1731 TCTGACAAACGATCGAGGACCGAAGGAGCTAACCGCTTTTTCACAACTGGGGGATCA 1672
Qy |||||
4434 TGTAACTCGCCTTGATCGTTGGGAAACCGAGCTGAATGAAGCCCATACCAACAGCAGCGG 4493
Db |||||
1671 TGTAACTCGCCTTGATCGTTGGGAAACCGAGCTGAATGAAGCCCATACCAACAGCAGCGG 1612
Qy |||||
4494 TGACACACGATGCTGAGCAATGGGCAACAACTGGGCAAACTATPAACTGGCGAACT 4553
Db |||||
1611 TGACACACGATGCTGAGCAATGGGCAACAACTGGGCAAACTATPAACTGGCGAACT 1552
Qy |||||
4554 ACTTACTCTAGCTTCCGGCAACAACTAATAGACTGGATGAGCGGATTAAGTTGCGAGG 4613
Db |||||
1551 ACTTACTCTAGCTTCCGGCAACAACTAATAGACTGGATGAGCGGATTAAGTTGCGAGG 1492
Qy |||||
4614 ACCACTTCTGGCTCGGCCCTTCGCGCTGGCTGTTTATGCTGATTAATCTGGAGCGGG 4673
Db |||||
1491 ACCACTTCTGGCTCGGCCCTTCGCGCTGGCTGTTTATGCTGATTAATCTGGAGCGGG 1432
Qy |||||
4674 TGAGCGTGGGTCTCGCGGTATCATGTCAGGACTGGGGCCAGATGATGAAGCCCTCCCGTAT 4733
Db |||||
1431 TGAGCGTGGGTCTCGCGGTATCATGTCAGGACTGGGGCCAGATGATGAAGCCCTCCCGTAT 1372
Qy |||||
4734 CGTAGTTATCTACAGCGGGGGGTTCAGGCACTATGGATGAACGAATAGACAGATCGC 4793
Db |||||
1371 CGTAGTTATCTACAGCGGGGGGTTCAGGCACTATGGATGAACGAATAGACAGATCGC 1312
Qy |||||
4794 TGAGATAGGTGCTCCTCACTGATTAAGCAATGGTAACTGTGAGCAACCAAGTTTACTCATATAT 4853
Db |||||
1311 TGAGATAGGTGCTCCTCACTGATTAAGCAATGGTAACTGTGAGCAACCAAGTTTACTCATATAT 1252
Qy |||||
4854 ACTTTAGATTGATTTAAACCTTCATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 4913
Db |||||
1251 ACTTTAGATTGATTTAAACCTTCATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 1192
Qy |||||
4914 TGATTAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGGTCAGACCC 4973
Db |||||
1191 TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGGTCAGACCC 1132
Qy |||||
4974 CGTAGAAAAGATCAAGGATCTCTTGTAGATCCTTTTCTGCGCGTAACTCTGCTGCTT 5033
Db |||||
1131 CGTAGAAAAGATCAAGGATCTCTTGTAGATCCTTTTCTGCGCGTAACTCTGCTGCTT 1072
Qy |||||
5034 GCAACCAAAAAACCAACCGCTTACAGCGGTGGTTTGTGCGGATCAAGAGCTACCAAC 5093
Db |||||
1071 GCAACCAAAAAACCAACCGCTTACAGCGGTGGTTTGTGCGGATCAAGAGCTACCAAC 1012

5094 TCTTTTCCGAAGTAACTGCTTTCAGCAGAGCGCAGATACCAAACTACTGCTCTCTAGT 5153
Db |||||
1011 TCTTTTCCGAAGTAACTGCTTTCAGCAGAGCGCAGATACCAAACTACTGCTCTCTAGT 952
Qy |||||
5154 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCTCATACCTCGCTCT 5213
Db |||||
951 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCTCATACCTCGCTCT 892
Qy |||||
5214 GCTAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAAGTCTGTTTACCGGTTTGA 5273
Db |||||
891 GCTAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAAGTCTGTTTACCGGTTTGA 832
Qy |||||
5274 CTCGAAGCAGATAGTTTACCGGATAAGCGCAGCGTTCGGGCTGAACGGGGGTTTCTGTCAC 5333
Db |||||
831 CTCGAAGCAGATAGTTTACCGGATAAGCGCAGCGTTCGGGCTGAACGGGGGTTTCTGTCAC 772
Qy |||||
5334 ACAGCCAGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCCTGAGCTATG 5393
Db |||||
771 ACAGCCAGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCCTGAGCTATG 712
Qy |||||
5394 AGAAGCGCCACGCTTCCGAGGAGGAGGCGACAGGTATCGGTAAAGCGCAGGCT 5453
Db |||||
711 AGAAGCGCCACGCTTCCGAGGAGGAGGCGACAGGTATCGGTAAAGCGCAGGCT 652
Qy |||||
5454 CGGAACAGGAGAGCGCAGCGGAGCTTCCAGGGGGGAAACCGCTTGTATCTTTATAGTCC 5513
Db |||||
651 CGGAACAGGAGAGCGCAGCGGAGCTTCCAGGGGGGAAACCGCTTGTATCTTTATAGTCC 592
Qy |||||
5514 TGTGCGGTTCGCCACCTCTGACTTGAGCGTTCGATTTTGTGATGCTCTGTCAGGGGGCG 5573
Db |||||
591 TGTGCGGTTCGCCACCTCTGACTTGAGCGTTCGATTTTGTGATGCTCTGTCAGGGGGCG 532
Qy |||||
5574 GAGCTATGAAAACCGCAGCAGCGGCTTTTACGGTTCCTGGCTTTTGTGCGC 5633
Db |||||
531 GAGCTATGAAAACCGCAGCAGCGGCTTTTACGGTTCCTGGCTTTTGTGCGC 472
Qy |||||
5634 TTTTGTCTACATGTTCTTCTGCTGTTATCCCTGATTTCTGTGATTAACCGTATTACCGC 5693
Db |||||
471 TTTTGTCTACATGTTCTTCTGCTGTTATCCCTGATTTCTGTGATTAACCGTATTACCGC 412
Qy |||||
5694 CTTTGTGAGTGAAGTATGATACCGCTCGCCGAGCGGAAACCGAGCGCGCAGTCAAGTGA 5753
Db |||||
411 CTTTGTGAGTGAAGTATGATACCGCTCGCCGAGCGGAAACCGAGCGCGCAGTCAAGTGA 352
Qy |||||
5754 CGAGAAAGCGAAGAGCGGCCCAATACGCAACCGGCTCTCCCGCGGTTGGCCGATTCA 5813
Db |||||
351 CGAGAAAGCGAAGAGCGGCCCAATACGCAACCGGCTCTCCCGCGGTTGGCCGATTCA 292
Qy |||||
5814 TTAATGCAG 5822
Db |||||
291 TTAATGCAG 283

RESULT 11
ADA94775/c
ID ADA94775 standard; DNA; 4514 BP.
XX
AC ADA94775;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid pGL2neo (+) #SEQ ID 4.
XX
KW Lymphocyte; vertebrate; antibody; genetically modified; ds.
XX
OS Synthetic.
XX
PN EP1321477-A1.
XX
PD 25-JUN-2003.
XX
PF 22-DEC-2001; 2001EP-00130805.
XX

PR 22-DEC-2001; 2001EP-00130805.
XX (GRAU/) GRAUNDER U.
PA (MELC/) MELCHERS G F.
XX
XX
XX Graunder U, Melchers GF;
XX
XX WPI; 2003-571360/54.
XX
XX Generating genetically modified vertebrate precursor lymphocytes for
PT producing any heterologous antibody or binding protein comprises
PT effecting differentiation of the precursor lymphocytes into mature
PT lymphoid lineage cells.
XX
XX Example 5; Page 49-51; 11pp; English.
XX
XX The invention relates to a method for generating vertebrate lymphocytes
CC that can be used for the production of any heterologous antibody, antigen
CC receptor, artificial binding protein, or their functional fragments. The
CC method of the invention comprises genetically modifying vertebrate
CC precursor lymphocytes, and effecting differentiation of the precursor
CC lymphocytes into mature lymphoid lineage cells either in vitro or in
CC vivo. The method and the genetically modified and differentiated
CC vertebrate lymphocytes are useful in the production of any heterologous
CC antibody, artificial binding protein, antigen receptor, or their
CC fragments, where the antibody is monoclonal or polyclonal, or partially
CC resembles a human antibody, binding protein or antigen receptor. The
CC antibodies are useful for the diagnosis, prevention and treatment of
CC diseases. The method combines the advantages of both the phage display
CC system (i.e. speed and flexibility in generating human antibodies, and
CC the ability to modify and improve the properties of existing antibodies),
CC and of the human immunoglobulin transgenic mouse technology (i.e. the
CC ability to obtain high affinity antibodies due to affinity maturation
CC occurring in the immune system, and the production antibodies with
CC physiologic and natural structural features). The current sequence
CC represents the plasmid sequence pGhzneo (+). This sequence is used in an
CC example from the invention as a template for the amplification of loxp
CC site flanked neomycin.
XX
XX Sequence 4514 BP; 1108 A; 1184 C; 1171 G; 1051 T; 0 U; 0 Other;

Query Match 45.8%; Score 2668.6; DB 8; Length 4514;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2677; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 3132 GGCCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGGTGTTTACAAAGTC 3191
DB |||||
QY 3192 GTGACTGGGAAACCCCTGGGTTACCCAACTTAATCGCCTTGACGACATGCCCTTTTCG 3251
DB |||||
QY 4454 GTGACTGGGAAACCCCTGGGTTACCCAACTTAATCGCCTTGACGACATGCCCTTTTCG 4395
DB |||||
QY 3252 CCAGCTGGGCTAATAGCAGGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTAC 3311
DB |||||
QY 4394 CCAGCTGGGCTAATAGCAGGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTAC 4335
DB |||||
QY 3312 TGAATGGCGAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTAC 3371
DB |||||
QY 4334 TGAATGGCGAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTAC 4275
DB |||||
QY 3372 GCGCAGCGTACCGCTTACCTTCCAGCGCCCTTAGCGCGGTCTCTTTTTCCTTTCC 3431
DB |||||
QY 4274 GCGCAGCGTGACCGCTTACCTTCCAGCGCCCTTAGCGCGGTCTCTTTTTCCTTTCC 4215
DB |||||
QY 3432 TTCCTTTCTCGCACGTTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTTT 3491
DB |||||
QY 4214 TTCCTTTCTCGCACGTTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTTT 4155
DB |||||
QY 3492 AGGGTTCCGATTTAGAGCTTTACGGCAGCTTCGACCGCAAAAACCTTGATTTGGGTGATGG 3551
DB |||||
QY 4154 AGGGTTCCGATTTAGAGCTTTACGGCAGCTTCGACCGCAAAAACCTTGATTTGGGTGATGG 4095
DB |||||

QY 3552 TTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCAC 3611
DB |||||
QY 4094 TTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCAC 4035
DB |||||
QY 3612 GTTCTTTAATAGTGGACTCTTGTTCMAACTGGAACAACTCAACCTATCTCGGTCTA 3671
DB |||||
QY 4034 GTTCTTTAATAGTGGACTCTTGTTCMAACTGGAACAACTCAACCTATCTCGGTCTA 3975
DB |||||
QY 3672 TTCCTTTGATTTAATAGGGATTTTTCGGCTATTTCGGCTATTGGTTAAAAAATGAGCTGAT 3731
DB |||||
QY 3974 TTCCTTTGATTTAATAGGGATTTTTCGGCTATTTCGGCTATTGGTTAAAAAATGAGCTGAT 3915
DB |||||
QY 3732 TTAACAAATATTTAACGCGAATTTTAAACAAATATTTAACGTTTACAAATTTTCGCCGTGATGC 3791
DB |||||
QY 3914 TTAACAAATATTTAACGCGAATTTTAAACAAATATTTAACGTTTACAAATTTTCGCCGTGATGC 3855
DB |||||
QY 3792 GGTATTTTCTCCTTAGCATCTGTGGGTATTTTTCACACCGCATACAGGTGGCATTTCG 3851
DB |||||
QY 3854 GGTATTTTCTCCTTAGCATCTGTGGGTATTTTTCACACCGCATACAGGTGGCATTTCG 3795
DB |||||
QY 3852 GGGAAATGTGCGCGGAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATCC 3911
DB |||||
QY 3794 GGGAAATGTGCGCGGAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATCC 3735
DB |||||
QY 3912 GCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTTGAAAAAGGAAGATGATGAG 3971
DB |||||
QY 3734 GCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTTGAAAAAGGAAGATGATGAG 3675
DB |||||
QY 3972 TATTCACATTTCCGTTGTCGCCCTTATTCCTTTTTCGGCAATTTTCCTTCTGTTTT 4031
DB |||||
QY 3674 TATTCACATTTCCGTTGTCGCCCTTATTCCTTTTTCGGCAATTTTCCTTCTGTTTT 3615
DB |||||
QY 4032 TGCTCACCCAGAAACCTGTGTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGT 4091
DB |||||
QY 3614 TGCTCACCCAGAAACCTGTGTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGT 3555
DB |||||
QY 4092 GGGTTACATCGAATCGAATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTTCGCCCCGAAGA 4151
DB |||||
QY 3554 GGGTTACATCGAATCGAATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTTCGCCCCGAAGA 3495
DB |||||
QY 4152 ACGTTTTTCCAATGATGAGACATTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTAT 4211
DB |||||
QY 3494 ACGTTTTTCCAATGATGAGACATTTTAAAGTTCTGCTATGTGTCATACATATATATCCCGTAT 3435
DB |||||
QY 4212 TGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTTGA 4271
DB |||||
QY 3434 TGACGCGCGGCAAGAGCAACTCGGTGCGCGCGCGGTATTCTCAGAAAGTACTTGGTTGA 3375
DB |||||
QY 4272 GTACTCACAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGTCAG 4331
DB |||||
QY 3374 GTACTCACAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGTCAG 3315
DB |||||
QY 4332 TGCTGCCATAACCATGAGTATAACACTCGGCCAACTTACTTCTGACAAAGATCGGAGG 4391
DB |||||
QY 3314 TGCTGCCATAACCATGAGTATAACACTCGGCCAACTTACTTCTGACAAAGATCGGAGG 3255
DB |||||
QY 4392 ACCGAAGAGTAAACCGCTTTTTCGACAACTGCGGGGATCATGTAACTCGCCTTGAATCG 4451
DB |||||
QY 3254 ACCGAAGAGTAAACCGCTTTTTCGACAACTGCGGGGATCATGTAACTCGCCTTGAATCG 3195
DB |||||
QY 4452 TTGGGAACCGAGCTGAATGAGCCATATCCAAACGACGAGCGTGACACAGATGCTGT 4511
DB |||||
QY 3194 TTGGGAACCGAGCTGAATGAGCCATATCCAAACGACGAGCGTGACACCAAGATGCTGT 3135
DB |||||
QY 4512 AGCAATGGCAACAACTGTGGCAAACTATTAACTGGCGAACTACTTACTTACTTCTCCG 4571
DB |||||
QY 3134 AGCAATGGCAACAACTGTGGCAAACTATTAACTGGCGAACTACTTACTTACTTCTCCG 3075
DB |||||
QY 4572 GCAACAATTAATAGACTGATGAGCGGATAAAGTTGACGACCACTTCTCGCGCTGGC 4631
DB |||||
QY 3074 GCAACAATTAATAGACTGATGAGCGGATAAAGTTGACGACCACTTCTCGCGCTGGC 3015
DB |||||
QY 4632 CCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGCGGTGAGCGGTCTCGCGG 4691
DB |||||

Db 3014 CTTTCGGGCTGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGTCTCGGG 2955
QY 4692 TATCATTCAGACACTGGGGCCAGATGTTAAAGCCCTCCCGTATCGTAGTTATCTACACGAC 4751
Db 2954 TATCATTCAGACACTGGGGCCAGATGTTAAAGCCCTCCCGTATCGTAGTTATCTACACGAC 2895
QY 4752 GGGGAGTCAGGCAACTATGAGTGAACGAAATAGACAGATCGTAGATAGTGCCTCACT 4811
Db 2894 GGGGAGTCAGGCAACTATGAGTGAACGAAATAGACAGATCGTAGATAGTGCCTCACT 2835
QY 4812 GATTAAGCATTTGTTAACTGTCAGACCAAGTTTACTCATATATATCTTAGATTGATTAAA 4871
Db 2834 GATTAAGCATTTGTTAACTGTCAGACCAAGTTTACTCATATATATCTTAGATTGATTAAA 2775
QY 4872 ACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTTGTATATCTCATGACCAA 4931
Db 2774 ACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTTGTATATCTCATGACCAA 2715
QY 4932 AATCCCTTAACTGAGTTTCTGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGG 4991
Db 2714 AATCCCTTAACTGAGTTTCTGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGG 2655
QY 4992 ATCTCTTTGAGATCCCTTTTCTCGCGGTAACTCTGCTGCTTGCATCAAAAAAACCCACC 5051
Db 2654 ATCTCTTTGAGATCCCTTTTCTCGCGGTAACTCTGCTGCTTGCATCAAAAAAACCCACC 2595
QY 5052 GCTACACGGGTGTTGTTGTCGGATCAAGAGCTACCACTCTTTTCCGAAAGGTAAAC 5111
Db 2594 GCTACACGGGTGTTGTTGTCGGATCAAGAGCTACCACTCTTTTCCGAAAGGTAAAC 2535
QY 5112 TGGCTTTAGCAGAGCGCAGATACCAATACCTGCTCTCTAGTGTAGCGGTAGAGGCA 5171
Db 2534 TGGCTTTAGCAGAGCGCAGATACCAATACCTGCTCTCTAGTGTAGCGGTAGAGGCA 2475
QY 5172 CCACCTCAAGAACTCTGTAGCACCGCCCTACATACCTCTGCTAATCTCTGTACCACT 5231
Db 2474 CCACCTCAAGAACTCTGTAGCACCGCCCTACATACCTCTGCTAATCTCTGTACCACT 2415
QY 5232 GGCTGCTCCAGTGGCGATAGTGTCTTACCGGGTTGAGCTCAAGACGATAGTTACC 5291
Db 2414 GGCTGCTCCAGTGGCGATAGTGTCTTACCGGGTTGAGCTCAAGACGATAGTTACC 2355
QY 5292 GGATAAGCGCAGCGGTCGGCTGAAACGGGGGTTCTGTCACACAGCCAGCTTGGAGCG 5351
Db 2354 GGATAAGCGCAGCGGTCGGCTGAAACGGGGGTTCTGTCACACAGCCAGCTTGGAGCG 2295
QY 5352 AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC 5411
Db 2294 AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC 2235
QY 5412 CGAAGGGAGAAAGCGGACAGGATTCGGTAAAGCGGCAAGGTTCGGAAACAGGAGCGCAC 5471
Db 2234 CGAAGGGAGAAAGCGGACAGGATTCGGTAAAGCGGCAAGGTTCGGAAACAGGAGCGCAC 2175
QY 5472 GAGGAGCTTCACGGGGGAAAGCGCTGTATCTTTATAGTCTCTGCGGTTTCGCCACT 5531
Db 2174 GAGGAGCTTCACGGGGGAAAGCGCTGTATCTTTATAGTCTCTGCGGTTTCGCCACT 2115
QY 5532 CTGACTTGAGCGTCAATTTTGTGATGCTCTGTCAGGGGGGCGAGCCCTATCGAAAAAGCG 5591
Db 2114 CTGACTTGAGCGTCAATTTTGTGATGCTCTGTCAGGGGGGCGAGCCCTATCGAAAAAGCG 2055
QY 5592 CAGCAACCGCGCTTTTACGGTCTCGGCTTTTGTGGCCCTTTTGTGTCACATGTTCTT 5651
Db 2054 CAGCAACCGCGCTTTTACGGTCTCGGCTTTTGTGGCCCTTTTGTGTCACATGTTCTT 1995
QY 5652 TCCTGCGTTATCCCTGATCTGTGATAACCGTATTTACCGCTTTTGTGAGCTGATAC 5711
Db 1994 TCCTGCGTTATCCCTGATCTGTGATAACCGTATTTACCGCTTTTGTGAGCTGATAC 1935
QY 5712 CGCTCGCGCAGCGCAACGACCGAGCGCAGCTAGTCAAGGAGGAGCGGAGAGCG 5771

Db 1934 CGCTCGCGCAGCGCAACGACCGAGCGCAGGTCAGTGAGCGAGCGAAGCG 1875
QY 5772 CCCAATAGCGAAACCGCTCTCCCGCGCGTGGCCGATTCATTATGACG 5822
Db 1874 CCCAATAGCGAAACCGCTCTCCCGCGCGTGGCCGATTCATTATGACG 1824
RESULT 12
ABK11039
ID ABK11039 standard; DNA; 9359 BP.
XX AC ABK11039;
XX AC ABK11039;
DT 05-JUN-2002 (first entry)
XX pVDH636 vector containing Arabidopsis Ath1 gene.
DE pVDH636 vector; circular; cyclic; grass; plant; herbicide resistance;
KW baseball; cricket; football; golf; rugby; soccer; tennis; lawn; park;
KW athletic field; animal feedstuff; grass flowering inhibitor; Ath1; gene;
KW ds.
XX Arabidopsis thaliana.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Oryza sativa.
OS Escherichia coli.
OS Cauliflower mosaic virus.
XX Synthetic.
FH Key Location/Qualifiers
FT CDS 4930..6360
FT /*tag= a
FT /product= "Ath1"
FT /partial
FT /note= "No stop codon"
XX WO200214524-A2.
PD 21-FEB-2002.
XX 16-AUG-2001; 2001WO-EP009572.
XX 18-AUG-2000; 2000US-0226422P.
PR 27-NOV-2000; 2000US-0253274P.
PR 27-NOV-2000; 2000US-0253327P.
PR 22-JUN-2001; 2001US-0300220P.
XX (ADVA-) ADVANTA SEEDS BV.
XX Van Der Valk P, Van Dun CMP, Smeekens SCM, Proveniers MCG;
XX WPI; 2002-257611/30.
XX P-PSDB; AAU76514.
XX New genetically modified grasses that express inhibited generative
propagation, or herbicide resistance, useful for forage (e.g. cattle
feedstuff) or amenity purposes (e.g. for use in an athletic field, lawn
or park).
XX Example 1; Fig 6; 56pp; English.
XX The invention relates to a grass plant, which has been genetically
modified to substantially inhibit generative propagation and carry
herbicide resistance. The grass is useful for growth and/or propagation
of grasses. The grass is used to play at least one sport (e.g. baseball,
cricket, football, golf, rugby, soccer or tennis), or used at least in a
portion of an athletic field, lawn or park. The grass is fed to animal
(e.g. cattle, goat, horse or sheep) or used as an animal feedstuff. The
present sequence represents the coding sequence of pVDH636 vector
containing the Arabidopsis Ath1 gene, which was used to inhibit flowering
in grasses

SQ	Sequence	9359 BP; 2377 A; 2222 C; 2133 G; 2624 T; 0 U; 3 Other;	
Query Match	45.7%;	Score 2658.4; DB 6; Length 9359;	
Best Local Similarity	99.7%;	Pred. No. 0;	
Matches 2685; Conservative	0; Mismatches	6; Indels	3; Gaps
2;			
QY	3129	TCGGGGCCAAATTCGGCCCTATAGTAGAGTCGATTAACAAATCACTGCGCGCTCGTTTACAAC	3188
Db	4	TCGGGGCCAAATTCGGCCCTATAGTAGAGTCGATTAACAAATCACTGCGCGCTCGTTTACAAC	63
QY	3189	GTGCTGACTGGGAAACCCCTGGGCTTACCCAACTTAATCGCCTTGCAGCACATCCGCCCTT	3248
Db	64	GTGCTGACTGGGAAACCCCTGGGCTTACCCAACTTAATCGCCTTGCAGCACATCCGCCCTT	123
QY	3249	TCGCCAGCTGGCTAATAGCGAGAGCGCGCACCGATCCGCCCTTCCCAACAGTTGGCA	3308
Db	124	TCGCCAGCTGGCTAATAGCGAGAGCGCGCACCGATCCGCCCTTCCCAACAGTTGGCA	183
QY	3309	GCCTGAATGGCGAATGAGCGCGCCCTGTAGCGCGCAATTAAGCGCGCGGCTGTGTGGT	3368
Db	184	GCCTGAATGGCGAATGAGCGCGCCCTGTAGCGCGCAATTAAGCGCGCGGCTGTGTGGT	243
QY	3369	TAGCGGAGCGTGACCGCTACACTTGCAGGCGCCTAGCGCCCTCTTTCGCTTCTT	3428
Db	244	TAGCGGAGCGTGACCGCTACACTTGCAGGCGCCTAGCGCCCTCTTTCGCTTCTT	303
QY	3429	CCCTTCCTTTCGCGCAGCTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCC	3488
Db	304	CCCTTCCTTTCGCGCAGCTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCC	363
QY	3489	TTTAGGCTTCGGATTAGAGCTTTACGGCACCTCGACCGCAAAACTTGATTTGGGTGA	3548
Db	364	TTTAGGCTTCGGATTAGAGCTTTACGGCACCTCGACCGCAAAACTTGATTTGGGTGA	423
QY	3549	TGFTACGAGTAGGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTC	3608
Db	424	TGFTACGAGTAGGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTC	483
QY	3609	CACGTCCTTTAATAGTAGGACTCTGTGTCCTCAACCTGGAAACACACTCAACCCCTATCTCGGT	3668
Db	484	CACGTCCTTTAATAGTAGGACTCTGTGTCCTCAACCTGGAAACACACTCAACCCCTATCTCGGT	543
QY	3669	CTATTCCTTTGATTTAAGGGATTTTGCAGTATTCGGCCCTATTGGTTAAAAAATGAGCT	3728
Db	544	CTATTCCTTTGATTTAAGGGATTTTGCAGTATTCGGCCCTATTGGTTAAAAAATGAGCT	603
QY	3729	GATTTAAACAAATTTAAACGGGAATTTTAAACAAATATTAACGTTTACAATTCGCCCTGA	3788
Db	604	GATTTAAACAAATTTAAACGGGAATTTTAAACAAATATTAACGTTTACAATTT--CCTGA	661
QY	3789	TGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCGCATACAGGTGGCCTTT	3848
Db	662	TGCGGTATTTCTCCTTACGCATCTGTGCGGTATTTACACCGCAT--CAGGTGGCCTTT	720
QY	3849	TCGGGGAAATGTCGCGGAAACCCCTATTGTTTATTTTCTTAAATATACATTCAAATATGTA	3908
Db	721	TCGGGGAAATGTCGCGGAAACCCCTATTGTTTATTTTCTTAAATATACATTCAAATATGTA	780
QY	3909	TCCGCTCATAGACAAATTAACCTGATTAATGCTTCAATAATTTGAAAAGGAAAGAGTAT	3968
Db	781	TCCGCTCATAGACAAATTAACCTGATTAATGCTTCAATAATTTGAAAAGGAAAGAGTAT	840
QY	3969	GAGTATTCAAATTTCCGCTGCGCCCTTATTCCTTTTTCGGGCAATTTGCTTCTCTGT	4028
Db	841	GAGTATTCAAATTTCCGCTGCGCCCTTATTCCTTTTTCGGGCAATTTGCTTCTCTGT	900
QY	4029	TTTTGCTCACCGAAGAACGCTGGTGAAGTAAAGATGCTGAAGATCAAGTTGGGTGACG	4088
Db	901	TTTTGCTCACCGAAGAACGCTGGTGAAGTAAAGATGCTGAAGATCAAGTTGGGTGACG	960
QY	4089	AGTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCCTGTAGAGTTTTCGCCCGGA	4148
Db	961	AGTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCCTGTAGAGTTTTCGCCCGGA	1020

Db	424	TGGTTACAGTAGTGGGCCATCGCCCTGATAGCGGTTTTTCGCCCTTTGACGTTGGAGTC	483
Qy	3609	CACGTTCTTTAAATAGTGGACTCTTTGTTCCAAACTGGAAACAACACTCAACCCCTATCTCGGT	3668
Db	484	CACGTCTTTAAATAGTGGACTCTTTGTTCCAAACTGGAAACAACACTCAACCCCTATCTCGGT	543
Qy	3669	CTATTCTTTGATTTAAGGGATTTTGGCGATTTTCGCCCTATTTGGTTAAAAATGAGCT	3728
Db	544	CTATTCTTTGATTTAAGGGATTTTGGCGATTTTCGCCCTATTTGGTTAAAAATGAGCT	603
Qy	3729	GAITTAACAAATATTTAAACGGAAATTTTAAACAAATATTTAAACGTTTACAAATTCGCGCTGA	3788
Db	604	GAITTAACAAAAATTTAAACGGAAATTTTAAACAAATATTTAAACGTTTACAAATTTTCTCTGA	661
Qy	3789	TGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACAGTGGCACTTTT	3848
Db	662	TGCGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACAGTGGCACTTTT	720
Qy	3849	TCGGGGAATGTGCGCGGAACCCCTATTTGTTTATTTTCTTAATACATTTCAATATGTA	3908
Db	721	TCGGGGAATGTGCGCGGAACCCCTATTTGTTTATTTTCTTAATACATTTCAATATGTA	780
Qy	3909	TCCGCTCATGAGACAATAACCTCATAAATGCTTTCAATAATATTTGAAAAAGGAGAGTAT	3968
Db	781	TCCGCTCATGAGACAATAACCTCATAAATGCTTTCAATAATATTTGAAAAAGGAGAGTAT	840
Qy	3969	GAGTATTTCAACATTTCCGTTGCGGCCCTTATTCCTCTTTTTTTCGCCATTTTGCCTTCCGT	4028
Db	841	GAGTATTTCAACATTTCCGTTGCGGCCCTTATTCCTCTTTTTTTCGCCATTTTGCCTTCCGT	900
Qy	4029	TTTTTGCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAG	4088
Db	901	TTTTTGCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAG	960
Qy	4089	AGTGGGTTACATCGAATCGATCTCAACAGCGTGAAGATCCTTGAGAGTTTTCGCCCGCA	4148
Db	961	AGTGGGTTACATCGAATCGATCTCAACAGCGTGAAGATCCTTGAGAGTTTTCGCCCGCA	1020
Qy	4149	AGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTATCCCG	4208
Db	1021	AGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTATCCCG	1080
Qy	4209	TATTGACCGCGGCAAGAGCAACTCGGTTCGCCGATACACTATTCTCAGAAATGACTTGGT	4268
Db	1081	TATTGACCGCGGCAAGAGCAACTCGGTTCGCCGATACACTATTCTCAGAAATGACTTGGT	1140
Qy	4269	TGAGTACTCACCAGTACAGAAAGATCTTACGGATGGCATGACAGTAAGAAATATG	4328
Db	1141	TGAGTACTCACCAGTACAGAAAGATCTTACGGATGGCATGACAGTAAGAAATATG	1200
Qy	4329	CAGTGTGCCATAACCATGATGATACACTTCGCCGCAACTTACTCTGACAAACGATCGG	4388
Db	1201	CAGTGTGCCATAACCATGATGATACACTTCGCCGCAACTTACTCTGACAAACGATCGG	1260
Qy	4389	AGNCCGAAGAGCTAACCGTTTTTTTGCAACAATGGGGATCATGTAACTCGCCTTGA	4448
Db	1261	AGNCCGAAGAGCTAACCGTTTTTTTGCAACAATGGGGATCATGTAACTCGCCTTGA	1320
Qy	4449	TCGTTGGGAACCGGAGCTGAATGAAGCATACCAACGACGAGCGTGCACACACGATGCC	4508
Db	1321	TCGTTGGGAACCGGAGCTGAATGAAGCATACCAACGACGAGCGTGCACACGATGCC	1380
Qy	4509	TGTAGCAATGGCAACAAGTTTGGCAAACTATTAACTTGGCGAATCTTACTAGCTTC	4568
Db	1381	TGTAGCAATGGCAACAAGTTTGGCAAACTATTAACTTGGCGAATCTTACTAGCTTC	1440
Qy	4569	CCGCCAACAAATTAAGACTGGATGGAGCGGATTAAGTTTGCAGGACCACTTCTGGCTC	4628
Db	1441	CCGCCAACAAATTAAGACTGGATGGAGCGGATTAAGTTTGCAGGACCACTTCTGGCTC	1500
Qy	4629	GGCCCTTCCGCTCGGCTGTTTATTGCTGATAAATCTGGAGCGGTGAGCGTGGTCTCG	4688

QY 5769 GGGCCAAATACGCAACCGCCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 5822
 DB 2641 GGGCCCAATACGCAACCGCCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 2694

RESULT 14
 ID ADA41728/c
 XX ADA41728 standard; DNA; 3404 BP.
 AC ADA41728;
 DT 20-NOV-2003 (first entry)
 XX
 DE Plasmid pUJO-20 DNA.
 XX
 KW RNA-dependent RNA polymerase; RdRP; plant virus; amplification system;
 KW ds; circular; cyclic.
 XX
 OS Synthetic.
 XX
 PN WO2003014366-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 29-JUL-2002; 2002WO-DE002863.
 XX
 PR 30-JUL-2001; 2001DE-01037444.
 XX
 FA (PROB-) PROBIOGEN AG.
 XX
 XX Sandig V, Jordan I;
 PI
 XX WPI; 2003-248302/24.
 XX

Amplifying nucleic acid in animal cells, useful e.g. for gene therapy or vaccination, uses an RNA-dependent, RNA-polymerase of a plant virus.

Example 2; Page 37-38; 39pp; German.

This invention describes a novel method for amplifying nucleic acid in animal cells by introducing an RNA-dependent RNA polymerase (RdRP) and its associated promoters and cis-acting signals from a plant virus into the cells. RdRP is normally active in plant cells and the gene that encodes it can be recovered from such cells. Both the RdRP and the promoter are from plant viruses, particularly turnip crinkle virus and the amplified RNA is a modified satellite or genomic RNA of this virus. The method is particularly used for amplification of RNA (which may be mRNA for protein synthesis; an effector, e.g. antisense RNA or ribozyme, or genomic RNA) in animal cells, for (i) control of gene expression or (ii) for gene therapy or vaccination. When the system includes an inducible promoter, it permits strong and rapid expression of reporter genes in response to a test substance, especially where the promoter responds to the human immune deficiency virus or heavy metals, to produce a diagnostic system or biosensor, respectively. The method of the invention provides an inducible or constitutive, autonomous RNA-dependent RNA amplification system for animal cells that requires only one polymerase and does not use any viral structural genes or helper viruses. Amplification takes place in the cytoplasm without using any components potentially infectious for the host cells. Human 293 cells were transformed with (i) pUJO-39, expressing a turnip crinkle virus 88 kD protein; (ii) pUJO-60, expressed satellite RNA-C of the same virus in the sense orientation and a fusion of internal ribosome entry site and green fluorescent protein in the antisense orientation, and (iii) an expression vector for T7 RNA polymerase under control of the cytomegalovirus promoter. Expression of the reporter gene was detected by fluorescence microscopy. This sequence represents a fragment of plasmid, pUJO-20 DNA used in the invention.

Sequence 3404 BP; 858 A; 853 C; 863 G; 830 T; 0 U; 0 Other;

Query Match 45.4%; Score 2641.4; DB 8; Length 3404;
 Best Local Similarity 99.7%; Pred. No. 0;

Matches 2668; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 3146 TATAGTAGTGTATTAACAATTCATGCGCGTCGTTTACAAACGTCGTGACCTGGGAAAAAC 3205
 DB |||||
 3404 TATAGTAGTGTATTAACAATTCATGCGCGTCGTTTACAAACGTCGTGACCTGGGAAAAAC 3345

QY 3206 CCTGGCGTTACCCAACTTAATCGCCTTCAGACACATCCCCCTTCGCCAGCTGGCGTAAT 3265
 DB |||||
 3344 CCTGGCGTTACCCAACTTAATCGCCTTCAGACACATCCCCCTTCGCCAGCTGGCGTAAT 3285

QY 3266 AGCGAAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCTGAATGGCGAATGG 3325
 DB |||||
 3284 AGCGAAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCTGAATGGCGAATGG 3225

QY 3326 AGCGCCCTGTAGCGGCGCATTAAGCGCGGGGTGTGGTGTAGCGCAGCGTGACCG 3385
 DB |||||
 3224 AGCGCCCTGTAGCGGCGCATTAAGCGCGGGGTGTGGTGTAGCGCAGCGTGACCG 3165

QY 3386 CTACACTTGGCCAGCGCCTTAGCGCCGCTCTCTTTCGCTTCTTCCCTTCTTCTTCTCGCA 3445
 DB |||||
 3164 CTACACTTGGCCAGCGCCTTAGCGCCGCTCTCTTTCGCTTCTTCCCTTCTTCTTCTCGCA 3105

QY 3446 CGTTCGCGGCTTTCGCCGTCAAAGCTCTAAATCGGGGGCTCCCTTTAGSGTTCCGATTTA 3505
 DB |||||
 3104 CGTTCGCGGCTTTCGCCGTCAAAGCTCTAAATCGGGGGCTCCCTTTAGSGTTCCGATTTA 3045

QY 3506 GAGCTTTAGGCACTCGACCGCAAAAACCTTGATTTGGGTGATGGTTCACGTAGTGGGC 3565
 DB |||||
 3044 GTGCTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATGGTTCACGTAGTGGGC 2985

QY 3566 CATGCGCCTGATAGACGGTCTTTCGCCCTTTCGAGCTTGAGTCCACGTTCTTTAATAGTG 3625
 DB |||||
 2984 CATGCGCCTGATAGACGGTCTTTCGCCCTTTCGAGCTTGAGTCCACGTTCTTTAATAGTG 2925

QY 3626 GACTCTTCTTCCAACTGGAACAAACACTCAACCCCTATCTCGTCTATCTTTTGGATTTAT 3685
 DB |||||
 2924 GACTCTTCTTCCAACTGGAACAAACACTCAACCCCTATCTCGTCTATCTTTTGGATTTAT 2865

QY 3686 AAGGATTTTCGGATTTTCGGCTTATTTGGTTAAAAAATGAGCTGATTTAAACAAATTTTA 3745
 DB |||||
 2864 AAGGATTTTCGGATTTTCGGCTTATTTGGTTAAAAAATGAGCTGATTTAAACAAATTTTA 2805

QY 3746 ACGGGAATTTTAAACAAATATTAAGTTTACAAATTTCCCTGATGGGTATTTTCTCCTT 3805
 DB |||||
 2804 ACGGGAATTTTAAACAAATATTAAGCTTACAAATTTTCTGATCGGTATTTTCTCCTT 2747

QY 3806 ACGCATCTGTGGGTATTTACACCGCATACAGGTGGCACTTTTCGGGGAATGTGGCGG 3865
 DB |||||
 2746 ACGCATCTGTGGGTATTTACACCGCATACAGGTGGCACTTTTCGGGGAATGTGGCGG 2688

QY 3866 GAACCCCTATTTGTTTATTTTCTTAAATACATTCAAATATGATATCCGCTCATGACAAAT 3925
 DB |||||
 2687 GAACCCCTATTTGTTTATTTTCTTAAATACATTCAAATATGATATCCGCTCATGACAAAT 2628

QY 3926 AACCTGATAATGCTTCAATAATTAACAAAGAGAGATGATGATTTCAACATTTCC 3985
 DB |||||
 2627 AACCTGATAATGCTTCAATAATTAACAAAGAGAGATGATGATTTCAACATTTCC 2568

QY 3986 GTGTCGCCCTTATTTCCCTTTTTCGGCATTTTCGCTTCTCTGTTTTCCTCACCCAGAAA 4045
 DB |||||
 2567 GTGTCGCCCTTATTTCCCTTTTTCGGCATTTTTCGCTTCTCTGTTTTCCTCACCCAGAAA 2508

QY 4046 CGCTGGTGAAGTAAAGATGCTGAAAGATCAGTTGGGTGACAGAGTGGGTTCATATCGAAC 4105
 DB |||||
 2507 CGCTGGTGAAGTAAAGATGCTGAAAGATCAGTTGGGTGACAGAGTGGGTTCATATCGAAC 2448

QY 4106 TGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCCGAGAGAGCTTTTCAATGA 4165
 DB |||||
 2447 TGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCCGAGAGAGCTTTTCAATGA 2388

QY 4166 TGAGCACTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCGCTATTGACCGCGGCAAG 4225
 DB |||||
 2387 TGAGCACTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCGCTATTGACCGCGGCAAG 2328

XX XX Example 9; Page 198-200; 241pp; English.

XX XX

CC CC The invention relates to a construct which allows animals to be bred in

CC CC captivity but renders them infertile in the wild by allowing reversible

CC CC control over fertility and reproduction. The construct comprises a native

CC CC promoter, a blocking DNA sequence contoured for and designed to abrogate

CC CC a crucial gene's function or to cause its mis-expression, and a genetic

CC CC switch to regulate controlled expression/repression of the blocker/gene

CC CC knockout. The construct is useful for preventing embryogenesis or

CC CC gametogenesis in animals by stably transforming an animal cell with the

CC CC construct by microinjection, transfection or infection, where the

CC CC construct stably integrates into the genome by homologous recombination,

CC CC and implanting the cell into a host organism, where a whole animal

CC CC develops from the implanted cell. The present DNA sequence is plasmid

CC CC construct pHSF70-1MCS used for transfection of Pacific oysters. The

CC CC plasmid contains *Drosophila* heat shock promoter 70 (dHSP70) and its poly

CC CC adenylation signal

XX XX

SO SO Sequence 3968 BP: 1075 A; 917 C; 943 G; 1033 T; 0 U; 0 Other;

Db	2168	AAAGGATCTTTCTTGAGATCCCTTTTTTTCTGGCGTAATCTGCTCTTGCRAACAAAAA	2109
Qy	5047	CCACCGGTACAGCGGTGGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTTCCGAAG	5106
Db	2108	CCACCGGTACAGCGGTGGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTTCCGAAG	2049
Qy	5107	GTAACCTGGCTTACAGAGCGCAGATACCAAACTCTCTCTCTAGTGTAGCCGTAGTTA	5166
Db	2048	GTAACCTGGCTTACAGAGCGCAGATACCAAACTCTCTCTCTAGTGTAGCCGTAGTTA	1989
Qy	5167	GGCCACCACTTCAGAACTCTGTAGACCGCCTACATACCTCGCTCTGCTAACTCTTTA	5226
Db	1988	GGCCACCACTTCAGAACTCTGTAGACCGCCTACATACCTCGCTCTGCTAACTCTTTA	1929
Qy	5227	CCAGTGGCTCTGCTGAGCGGTAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAG	5286
Db	1928	CCAGTGGCTCTGCTGAGCGGTAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAG	1869
Qy	5287	TTACCGGATTAAGCGGCGAGCGGTCCGGCTGAAACGGGGGGTTCGTGCAACAGCCAGCTTG	5346
Db	1868	TTACCGGATTAAGCGGCGAGCGGTCCGGCTGAAACGGGGGGTTCGTGCAACAGCCAGCTTG	1809
Qy	5347	GAGCGACGACCTACACCGACTGAGATACCTACAGCGTGAAGTCTGAGAAAGGCCACG	5406
Db	1808	GAGCGACGACCTACACCGACTGAGATACCTACAGCGTGAAGTCTGAGAAAGGCCACG	1749
Qy	5407	CTTCCCGAAGGGGAAAGCGGACAGGTATCCGGTAAGCGGCGGGTCCGAAACAGGAGAG	5466
Db	1748	CTTCCCGAAGGGGAAAGCGGACAGGTATCCGGTAAGCGGCGGGTCCGAAACAGGAGAG	1689
Qy	5467	CGACAGGAGGAGCTTCCAGGGGAAACGCTGGTATCTTTATAGTCTGTCGGGTTTCGC	5526
Db	1688	CGACAGGAGGAGCTTCCAGGGGAAACGCTGGTATCTTTATAGTCTGTCGGGTTTCGC	1629
Qy	5527	CACCTCTGACTGAGCGTCTGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTATGGAAA	5586
Db	1628	CACCTCTGACTGAGCGTCTGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTATGGAAA	1569
Qy	5587	AAGCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGGTGGCCCTTTTGTCTACATG	5646
Db	1568	AAGCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGGTGGCCCTTTTGTCTACATG	1509
Qy	5647	TTCTTTCTCGGTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTAGTGAGCT	5706
Db	1508	TTCTTTCTCGGTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTAGTGAGCT	1449
Qy	5707	GATACCGCTCGCGCAGCGAAGCAGCGAGCGAGTCACTGAGCGAGGAGCGGAA	5766
Db	1448	GATACCGCTCGCGCAGCGAAGCAGCGAGCGAGTCACTGAGCGAGGAGCGGAA	1389
Qy	5767	GAGCGCCCAATACGCAACCGCCTCTCCCGCGGTTGGCCGATTTCATTAAATGAG	5822
Db	1388	GAGCGCCCAATACGCAACCGCCTCTCCCGCGGTTGGCCGATTTCATTAAATGAG	1333

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 14:03:42 ; Search time 263 Seconds
(without alignments)
12284.882 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagcagcaggttcccg.....tgccgattcattaatgcag 5822

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2755.6	47.3	5534	1	US-08-452-267-3
2	2755.6	47.3	5534	3	US-09-123-644-3
3	2630.4	45.2	3485	4	US-08-939-366-10
4	2553	43.9	4965	3	US-08-675-566-22
5	2553	43.9	5109	3	US-08-675-566-19
6	2553	43.9	6196	3	US-08-675-566-5
7	2553	43.9	6243	3	US-08-675-566-14
8	2553	43.9	6503	3	US-08-675-566-6
9	2553	43.9	6958	3	US-08-675-566-2
10	2553	43.9	7379	3	US-08-675-566-13
11	2553	43.9	8618	3	US-08-675-566-21
12	2553	43.9	8792	3	US-08-675-566-25
13	2550	43.8	4883	4	US-09-608-730B-21
14	2550	43.8	7287	2	US-08-659-206A-1
15	2549	43.8	6345	2	US-08-472-809B-7
16	2545.8	43.7	6045	3	US-08-675-566-18
17	2545.8	43.7	6244	3	US-08-675-566-17
18	2545.8	43.7	6447	3	US-08-675-566-16
19	2545.8	43.7	6612	3	US-08-675-566-15
20	2533.4	43.5	5585	2	US-08-305-221-1
21	2533.4	43.5	5585	4	US-09-000-003A-1
22	2532	43.5	7432	4	US-09-367-891A-6
23	2515	43.2	13910	3	US-09-263-933-1
24	2515	43.2	13910	3	US-08-263-933-8
25	2515	43.2	13910	3	US-09-263-933-15
26	2515	43.2	13910	4	US-09-919-901-1
27	2515	43.2	13910	4	US-09-919-901-8

28 2515 43.2 13910 4 US-09-919-901-15 Sequence 15, Appli
29 2483.8 42.7 7659 3 US-09-128-314-4 Sequence 4, Appli
30 2483.8 42.7 8157 3 US-09-128-314-3 Sequence 3, Appli
31 2460.6 42.3 2927 2 US-08-941-647A-1 Sequence 1, Appli
32 2460.6 42.3 2927 4 US-09-143-481-14 Sequence 14, Appli
33 2429.6 41.7 5261 4 US-09-770-315-7 Sequence 7, Appli
34 2414 41.5 4118 4 US-09-068-821-17 Sequence 17, Appli
35 2414 41.5 4118 4 US-09-068-821-18 Sequence 18, Appli
36 2326.2 40.0 5248 4 US-08-487-283A-18 Sequence 18, Appli
37 2326.2 40.0 5248 5 PCT-US96-05611A-21 Sequence 21, Appli
38 2326.2 40.0 5443 2 US-08-929-967-1 Sequence 1, Appli
39 2326.2 40.0 5616 2 US-08-929-967-3 Sequence 3, Appli
40 2326.2 40.0 6619 2 US-08-683-007A-3 Sequence 3, Appli
41 2326.2 40.0 7375 4 US-09-513-442-1 Sequence 1, Appli
42 2324 39.9 4776 4 US-09-287-368-7 Sequence 7, Appli
43 2320 39.8 6714 1 US-08-021-623C-5 Sequence 5, Appli
44 2318.6 39.8 3664 1 US-08-148-675A-1 Sequence 1, Appli
45 2313.8 39.7 6371 2 US-08-715-808-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-452-267-3
; Sequence 3, Application US/08452267
; Patent No. 5801027
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Ramsey, Nichola
; TITLE OF INVENTION: Control of Genes in Transgenic Plants
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 South Meridian
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,267
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P.
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 6653-25744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: PUMIGIT
; US-08-452-267-3

Query Match 47.3%; Score 2755.6; DB 1; Length 5534;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2890; Conservative 0; Mismatches 38; Indels 74; Gaps 4;

Db	4471	AAAGTCAAAGGATCTTCTTGAGATCCCTTTTTTCTGCGCGTAATCTGCTGCTTGC	AAACA	45310
Qy	5041	AAAAAACCCAGCTACACAGCGGTGGTTGGTTGGCGGATCAAGAGCTACCAATCTCTTTT		5100
Db	4531	AAAAAACCCAGCTACACAGCGGTGGTTGGTTGGCGGATCAAGAGCTACCAATCTCTTTT		4590
Qy	5101	CCGAGGTAACTGGCTTCAGCAGAGCCGAGATACCAAAATCTGTCCTTCAGTGTAGCCG		5160
Db	4591	CCGAGGTAACTGGCTTCAGCAGAGCCGAGATACCAAAATCTGTCCTTCAGTGTAGCCG		4650
Qy	5161	TAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATC		5220
Db	4651	TAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATC		4710
Qy	5221	CTGTTACCATGCGTGTGCGAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGA		5280
Db	4711	CTGTTACCATGCGTGTGCGAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGA		4770
Qy	5281	CGATAGTTACCGGATAGCGCAGCGTGGGCTGAACCGGGGGTTCGTGCAACAGCCCC		5340
Db	4771	CGATAGTTACCGGATAGCGCAGCGTGGGCTGAACCGGGGGTTCGTGCAACAGCCCC		4830
Qy	5341	AGCTTGAGCGAAACGACTACCGAACTCAGATACCTACAGCGTGAGCTATCAGAAAGC		5400
Db	4831	AGCTTGAGCGAAACGACTACCGAACTCAGATACCTACAGCGTGAGCTATCAGAAAGC		4890
Qy	5401	GCCACGCTTCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGTCGAAACA		5460
Db	4891	GCCACGCTTCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGTCGAAACA		4950
Qy	5461	GGAGAGCGCACGAGGAGCTTCCAGGGGGAAACGCTGGTGATCTTTATAGTCTGTGCGG		5520
Db	4951	GGAGAGCGCACGAGGAGCTTCCAGGGGGAAACGCTGGTGATCTTTATAGTCTGTGCGG		5010
Qy	5521	TTTTCGGCACTCTGACCTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCCTA		5580
Db	5011	TTTTCGGCACTCTGACCTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCCTA		5070
Qy	5581	TGGAATAACGCCAGCAACGGCGCTTTTACGGTTCTTGCGCTTTTGCTGGCCCTTTGCT		5640
Db	5071	TGGAATAACGCCAGCAACGGCGCTTTTACGGTTCTTGCGCTTTTGCTGGCCCTTTGCT		5130
Qy	5641	CACATGTTCTTCTCGCTTATCCCTCGATTCGTGGAATAACCGCTATTACCGCTTTGAG		5700
Db	5131	CACATGTTCTTCTCGCTTATCCCTCGATTCGTGGAATAACCGCTATTACCGCTTTGAG		5190
Qy	5701	TGAGCTTGATACCGCTTCGCGCAGCCGAAACGACGAGCGCAGCGAGTCAGTGACGAGGAA		5760
Db	5191	TGAGCTTGATACCGCTTCGCGCAGCCGAAACGACGAGCGCAGCGAGTCAGTGACGAGGAA		5250
Qy	5761	GGGGAAGAGCGCCCAATACGCAAAACGCTCTCTCCCGCGCTTGGCCGATTCAATATCG		5820
Db	5251	GGGGAAGAGCGCCCAATACGCAAAACGCTCTCTCCCGCGCTTGGCCGATTCAATATCG		5310
Qy	5821	AG 5822		
Db	5311	AG 5312		

RESULT 2

```

US-09-123-644-3
; Sequence 3, Application US/09123644
; Patent No. 6127606
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Ramsay, Nicola
; TITLE OF INVENTION: Method of Using Transactivation Proteins to
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 South Meridian
; CITY: Indianapolis

```

Db	2906	GTTGTTACGGCGAGCGTGACCGCTACACTTGGCCAGCGCCCTAGCGCGCTCTCTTC	2965	3931	CGCTTTGATCGTTGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACC	3990
Qy	3421	GCTTTCTCCCTTCTCTTCTCGCCACGCTTGGCGCGCTTCCCGCTCAAGCTCTAAATCGG	3480	4501	ACGATCCCTGTAGCAATGCAACACAGCTTGGCGCAAACTATTAACTGCGCAACTACTTACT	4560
Db	2966	GCTTTCTCCCTTCTCTTCTCGCCACGCTTGGCGCGCTTCCCGCTCAAGCTCTAAATCGG	3025	3991	ACGATCCCTGTAGCAATGCAACACAGCTTGGCGCAAACTATTAACTGCGCAACTACTTACT	4050
Qy	3481	GGGCTCCCTTTAGGTTCCGATTTAGAGCTTTACGGCACTTCGACCGCAAAACTTGTAT	3540	4561	CTAGCTTCCCGGCAACAAATTAATAGACTGGATCGAGCGGATAAAGTTGCGAGCACACTT	4620
Db	3026	GGGCTCCCTTTAGGTTCCGATTTAGAGCTTTACGGCACTTCGACCGCAAAACTTGTAT	3085	4051	CTAGCTTCCCGGCAACAAATTAATAGACTGGATCGAGCGGATAAAGTTGCGAGCACACTT	4110
Qy	3541	TTGGGTGATGGTTCAAGTAGTGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGAAG	3600	4621	CTCGGCTCGGCCCTTCGGCTGGCTGTTTATTGCTGATAAATCTGAGCGCGGTAGCGGT	4680
Db	3086	TAGGGTGAUGTTTCAAGTAGTGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGAAG	3145	4111	CTCGGCTCGGCCCTTCGGCTGGCTGTTTATTGCTGATAAATCTGAGCGCGGTAGCGGT	4170
Qy	3601	TTGGAGTCCAGCTTCTTTAATAGTGAATCTTGTTCGAATCTGGAACAACTCAACCTT	3660	4681	GGGTCTCGCGGTATCATTTGAGCACTGGGCGCCAGATGGTAAAGCCCTCCCGTATCGTAGTT	4740
Db	3146	TTGGAGTCCAGCTTCTTTAATAGTGAATCTTGTTCGAATCTGGAACAACTCAACCTT	3205	4171	GGGTCTCGCGGTATCATTTGAGCACTGGGCGCCAGATGGTAAAGCCCTCCCGTATCGTAGTT	4230
Qy	3661	ATCTCGGCTATTTCTTTGATTTATAGGATTTTTCGGATTTTCGGCTATTGGTTAAAA	3720	4741	ATCTACAGCGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATA	4800
Db	3206	ATCTCGGCTATTTCTTTGATTTATAGGATTTTTCGGATTTTCGGCTATTGGTTAAAA	3265	4231	ATCTACAGCGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATA	4290
Qy	3721	AATGAGCTGATTTAAACAAATTTTAAACCGAATTTTAAACAAATTTTAAACCTTTTAAAT	3780	4801	GGTGCTCTCACTGATTAAGCAATTTGTAACCTCTCAGACCAAGTTTACTCATATATACTTTAG	4860
Db	3266	AATGAGCTGATTTAAACAAATTTTAAACCGAATTTTAAACAAATTTTAAACCTTTTAAAT	3325	4291	GGTGCTCTCACTGATTAAGCAATTTGTAACCTCTCAGACCAAGTTTACTCATATATACTTTAG	4350
Qy	3781	TGGCTGATGGGTTATTTCTCTTACGATCTGTGGGTTATTTCAACCGCATACAGGT	3840	4861	ATTGATTTAAAACTTCAATTTTAAAGGATCTTAGGTGAAGATCTTTTGTGATAAT	4920
Db	3326	T-----AGGT	3330	4351	ATTGATTTAAAACTTCAATTTTAAAGGATCTTAGGTGAAGATCTTTTGTGATAAT	4410
Qy	3841	GGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTATTTCTAAATACTTCA	3900	4921	CTCATGACCAAAATCCCTTAAACGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA	4980
Db	3331	GGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTATTTCTAAATACTTCA	3390	4411	CTCATGACCAAAATCCCTTAAACGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA	4470
Qy	3901	AATATGATCGCTCATGAGCAATAACCCCTGATAATTCCTCAATAATTTGAAAAAGG	3960	4981	AAGATCAAGAGATCTTCTTGAGATCTTTTCTGCGCGTAACTCTGCTGCTTCCAAACA	5040
Db	3391	AATATGATCGCTCATGAGCAATAACCCCTGATAATTCCTCAATAATTTGAAAAAGG	3450	4471	AAGATCAAGAGATCTTCTTGAGATCTTTTCTGCGCGTAACTCTGCTGCTTCCAAACA	4530
Qy	3961	AAGATGATGATTTCAACATTTCTGCTGCGCCCTTATCCCTTTTTCGGGCAATTTGC	4020	5041	AAAAAACACCGCTTACCAGCGGTGGTTTGTTCGGGATCAAGAGCTACCAACTCTTTTT	5100
Db	3451	AAGATGATGATTTCAACATTTCTGCTGCGCCCTTATCCCTTTTTCGGGCAATTTGC	3510	4531	AAAAAACACCGCTTACCAGCGGTGGTTTGTTCGGGATCAAGAGCTACCAACTCTTTTT	4590
Qy	4021	CTTCTGTTTTGCTCAACCAAGAAACGCTGCTGAAAGTAAAGATGCTGAAGATCAGTTG	4080	5101	CCGAAGGTAACTGGCTTACGAGAGCGCAGATACCAATACTGCTCTCTAGTGTAGCGG	5160
Db	3511	CTTCTGTTTTGCTCAACCAAGAAACGCTGCTGAAAGTAAAGATGCTGAAGATCAGTTG	3570	4591	CCGAAGGTAACTGGCTTACGAGAGCGCAGATACCAATACTGCTCTCTAGTGTAGCGG	4650
Qy	4081	GGTGACGAGTGGTTATCATCGAACTGGATCTCAACAGCGGTAAGATCTCTTGAGGTTTT	4140	5161	TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTCATACCTCGCTCTGCTAATC	5220
Db	3571	GGTGACGAGTGGTTATCATCGAACTGGATCTCAACAGCGGTAAGATCTCTTGAGGTTTT	3630	4651	TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTCATACCTCGCTCTGCTAATC	4710
Qy	4141	CGCCCGAGAAACGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGTA	4200	5221	CTGTTTACAGTGGCTGCTGCGCAGTGGCGATAAGTCTGTTACCGGTTGGAATCAAGA	5280
Db	3631	CGCCCGAGAAACGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGTA	3690	4711	CTGTTTACAGTGGCTGCTGCGCAGTGGCGATAAGTCTGTTACCGGTTGGAATCAAGA	4770
Qy	4201	TTATCCGCTATGACCGCGGCAAGACAACTCGGTGCGCCGATACACTATTCTCAGAAAT	4260	5281	CGATAGTTACCGGATAGGCGCAGCGTTCGGGCTGAAACGGGGGTTCTGTGACACAGGCC	5340
Db	3691	TTATCCGCTATGACCGCGGCAAGACAACTCGGTGCGCCGATACACTATTCTCAGAAAT	3750	4771	CGATAGTTACCGGATAGGCGCAGCGTTCGGGCTGAAACGGGGGTTCTGTGACACAGGCC	4830
Qy	4261	GACTTGTGTAGTACTACAGTACAGAAAGCACTTTAAGGATGCGATGACAGTAAAGA	4320	5341	AGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTTACAGCGGTGAGCTATGAGAAAGC	5400
Db	3751	GACTTGTGTAGTACTACAGTACAGAAAGCACTTTAAGGATGCGATGACAGTAAAGA	3810	4831	AGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTTACAGCGGTGAGCTATGAGAAAGC	4890
Qy	4321	GAATATGAGTGTGCGCATACCAATGATGATGATGATGATGATGATGATGATGATGATGAT	4380	5401	GCCACGCTTCCGAGGAGGAAAGCGGACAGGTATCCGGTAAAGCGGCGAGGTCGGAACA	5460
Db	3811	GAATATGAGTGTGCGCATACCAATGATGATGATGATGATGATGATGATGATGATGATGAT	3870	4891	GCCACGCTTCCGAGGAGGAAAGCGGACAGGTATCCGGTAAAGCGGCGAGGTCGGAACA	4950
Qy	4381	ACGATCGGAGGACCGAAGGATCTTACCGCTTTTTCGCAACATGCGGGGATCATGTAAT	4440	5461	GGAGAGCGCAGGAGGATCTTCCAGGGGAAACGCTCGGTATCTTTATAGTCTCTCGGG	5520
Db	3871	ACGATCGGAGGACCGAAGGATCTTACCGCTTTTTCGCAACATGCGGGGATCATGTAAT	3930	4951	GGAGAGCGCAGGAGGATCTTCCAGGGGAAACGCTCGGTATCTTTATAGTCTCTCGGG	5010
Qy	4441	CGCTTGTATCGGTTGGAAACCGGAGCTGATGAGCCATACCAACGACGAGCGTGACACC	4500	5521	TTTTCGCCACCTCTGACTTGAAGCTCGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTTA	5580
Db		CGCTTGTATCGGTTGGAAACCGGAGCTGATGAGCCATACCAACGACGAGCGTGACACC		5011	TTTTCGCCACCTCTGACTTGAAGCTCGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTTA	5070

QY 5581 TGAAGAAAGCGGAGCAACGCGGCTTTTACGGTTCTCGCCTTTTGCTGGCCTTTTGCT 5640
Db TGAAGAAAGCGGAGCAACGCGGCTTTTACGGTTCTCGCCTTTTGCTGGCCTTTTGCT 5130
QY 5641 CACATGTTCTTCTCGGTTATCCCGTATCTCGTATCTGTGGAATAACCGTATACCGCCTTTGAG 5700
Db CACATGTTCTTCTCGGTTATCCCGTATCTCGTATCTGTGGAATAACCGTATACCGCCTTTGAG 5190
QY 5701 TGAGCTGATACCGCTCGCGGAGCGGAACGAGCGGAGCGAGTCACTGAGCGAGGAA 5760
Db TGAGCTGATACCGCTCGCGGAGCGGAACGAGCGGAGCGAGTCACTGAGCGAGGAA 5250
QY 5761 GCGGAAGAGCGGCCCAATAGCAAAACGCGCTCTCCCGCGCGTTGGCCGATTCAATTAATCC 5820
Db GCGGAAGAGCGGCCCAATAGCAAAACGCGCTCTCCCGCGCGTTGGCCGATTCAATTAATCC 5310
QY 5821 AG 5822
Db 5311 AG 5312

RESULT 3

US-08-939-366-10/c
; Sequence 10, Application US/08939366
; Patent No. 6355415
; GENERAL INFORMATION:
; APPLICANT: Wagner, Thomas E.
; APPLICANT: Xie, Yuesheng
; TITLE OF INVENTION: Compositions and Methods for the Use of
; TITLE OF INVENTION: Ribozymes to Determine Gene Function
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,366
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02749
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3485 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-939-366-10

Query Match 45.2%; Score 2630.4; DB 4; Length 3485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2671; Conservative 0; Mismatches 31; Indels 2; Gaps 2;
QY 3119 GCATGCGACGTCGGGCGGCAATTCGCCCTATAGTGTGATTAACAATTCATCTGGCGGTC 3178
Db 3318 GCATGCGACGTCGGGCGGCAATTCGCCCTATAGTGTGATTAACAATTCATCTGGCGGTC 3259

QY 3179 GTTTTACACGCTCGTACCTGGGAAACCTTGGGTTACCCAACTTAATCGCCTTGCAGCA 3238
Db TTTTACACGCTCGTACCTGGGAAACCTTGGGTTACCCAACTTAATCGCCTTGCAGCA 3200
QY 3239 CATCCCGCTTTTCGCGAGCTGTAATAGCAAGAGGCGCGACCATCGCCTTCCCAA 3298
Db CATCCCGCTTTTCGCGAGCTGG-GTAATAGCAAGAGGCGCGACCATCGCCTTCCCAA 3141
QY 3299 CAGTTGCGCAGCTGAAATGGCGAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGCGG 3358
Db CAGTTGCGCAGCTGAAATGGCGAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGCGG 3081
QY 3359 GTGTGCTGTACGCGCAGCGTACGCTACACTTGCAGCGCGCCTAGCGCGCTCCTT 3418
Db GTGTGCTGTACGCGCAGCGTACGCTACACTTGCAGCGCGCCTAGCGCGCTCCTT 3021
QY 3419 TCGCTTTCTTCCTTCTCGGCAAGTTCGCGCGCTTCCCGCTCAAGCTCTAAATC 3478
Db TCGCTTTCTTCCTTCTCGGCAAGTTCGCGCGCTTCCCGCTCAAGCTCTAAATC 2961
QY 3479 GGGGCTCCCTTTAGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTG 3538
Db GGGGCTCCCTTTAGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTG 2901
QY 3539 ATTTGGGTGATGTTACGCTAGTGGCCATCGCCCTGATAGCGGTTTTTCGCCCTTTGA 3598
Db ATTTGGGTGATGTTACGCTAGTGGCCATCGCCCTGATAGCGGTTTTTCGCCCTTTGA 2841
QY 3599 CGTTGGAGTCCACGCTTCTTTAATAGTGACCTTCTTCCAAACTGGAACACACCTCAACC 3658
Db CGTTGGAGTCCACGCTTCTTTAATAGTGACCTTCTTCCAAACTGGAACACACCTCAACC 2781
QY 3659 CTATCTCGGTCTATCTTTTGAATTAAGGATTTTCGCGATTTTCGCCCTATTGGTTAA 3718
Db CTATCTCGGTCTATCTTTTGAATTAAGGATTTTCGCGATTTTCGCCCTATTGGTTAA 2721
QY 3719 AAAATGAGCTGATTAACAAATATTAACGGAATTTTAAACAAATATTAACGTTTAA 3778
Db AAAATGAGCTGATTAACAAATATTAACGGAATTTTAAACAAATATTAACGTTTAA 2661
QY 3779 TTTCCGCTGATCGGCTATTTCTCTTACGCTATCTGTGCGGTTTTCACCGGATACAG 3838
Db TTTCCGCTGATCGGCTATTTCTCTTACGCTATCTGTGCGGTTTTCACCGGATACAG 2601
QY 3839 GTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACAT 3898
Db GTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACAT 2541
QY 3899 CAAATATGATCCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATATTGAAAAA 3958
Db CAAATATGATCCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATATTGAAAAA 2481
QY 3959 GGAAGAGTATGAGTATTAACATTTCCGCTGTGCGCCTTATTCCCTTTTTCGGCATTT 4018
Db GGAAGAGTATGAGTATTAACATTTCCGCTGTGCGCCTTATTCCCTTTTTCGGCATTT 2421
QY 4019 GCCTTCCTGTTTTGCTCACCCAGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGT 4078
Db GCCTTCCTGTTTTGCTCACCCAGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGT 2361
QY 4079 TGGGTGACGAGTGGTTTACATCGAACTGATCTCAACAGCGGTAAAGATCTTGAAGATT 4138
Db TGGGTGACGAGTGGTTTACATCGAACTGATCTCAACAGCGGTAAAGATCTTGAAGATT 2301
QY 4139 TTGCCCCCGGAAGAACGTTTTTCCATGATGAGCACTTTTAAAGTTCTCTATGTGCGCGG 4198
Db TTGCCCCCGGAAGAACGTTTTTCCATGATGAGCACTTTTAAAGTTCTCTATGTATACAC 2241
QY 4199 TATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGA 4258
Db TATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCGCGGTATTCTCACA 2181
QY 4259 ATGACTTGGTTGAGTACTTACCAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAA 4318

Db 2180 ATGACTTGGTTGAGTACTACCAAGTACAGAAAGCATCTTACGATGGCATGACAGTAA 2121
QY GAGAAATATGCAAGTGTGCGCATACCAATGAGTGAATACATCTGCGGCAACTTACTTCTGA 4378
Db 2120 GAGAAATATGCAAGTGTGCGCATACCAATGAGTGAATACATCTGCGGCAACTTACTTCTGA 2061
QY CACAGATCGGAGGACCGAAGGAGTAAACCGCTTTTGTGCAAAACATCGGGGATCATGTAA 4438
Db 2060 CACAGATCGGAGGACCGAAGGAGTAAACCGCTTTTGTGCAAAACATCGGGGATCATGTAA 2001
QY CTGCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGCGTGA 4498
Db 2000 CTGCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGCGTGA 1941
QY CCACGATGCTGTAGCAATGGCAACAGCTTGGCAAACTATTAACTGGGGAATCTCTTA 4558
Db 1940 CCACGATGCTGTAGCAATGGCAACAGCTTGGCAAACTATTAACTGGGGAATCTCTTA 1881
QY CTCTAGCTTCCCGCAACAAATTAATAGACTGGATGGAGGGGATAAAGTTGCAGGACCA 4618
Db 1880 CTCTAGCTTCCCGCAACAAATTAATAGACTGGATGGAGGGGATAAAGTTGCAGGACCA 1821
QY TTCTGCGCTCGGCCCTTCCGCTCGCTGGTTTATTGTGTGAATAATCTGGAGCCGGTGAGC 4678
Db 1820 TTCTGCGCTCGGCCCTTCCGCTCGCTGGTTTATTGTGTGAATAATCTGGAGCCGGTGAGC 1761
QY GTGGGTCTCGCGGTATCTGACAGCTGGGGCCAGATGTTAAGCCCTCCCGTATCTGAG 4738
Db 1760 GTGGGTCTCGCGGTATCTGACAGCTGGGGCCAGATGTTAAGCCCTCCCGTATCTGAG 1701
QY TTATCTACACGACGGGAGTCAGGCACTATGGATGAACGAATAGACAGATCGCTGAGA 4798
Db 1700 TTATCTACACGACGGGAGTCAGGCACTATGGATGAACGAATAGACAGATCGCTGAGA 1641
QY TAGTGTGCTCTACTGATTAAGCAATGGTAAGTGTGAGCAAGTGTGATCATATATATCTTT 4858
Db 1640 TAGTGTGCTCTACTGATTAAGCAATGGTAAGTGTGAGCAAGTGTGATCATATATATCTTT 1581
QY AGATTGATTAAGCAATGGTAAGTGTGAGCAAGTGTGATCATATATATCTTTTGA 4918
Db 1580 AGATTGATTAAGCAATGGTAAGTGTGAGCAAGTGTGATCATATATATCTTTTGA 1521
QY ATCTCATGACCAAAATCCCTTAACTGAGTGTGATGATGATGATGATGATGATGATGATG 4978
Db 1520 ATCTCATGACCAAAATCCCTTAACTGAGTGTGATGATGATGATGATGATGATGATG 1461
QY AAAAGATCAAAAGGATCTTCTTGAATCCTTTTCTGCGGTAAATCTGCTGCTTGGAAA 5038
Db 1460 AAAAGATCAAAAGGATCTTCTTGAATCCTTTTCTGCGGTAAATCTGCTGCTTGGAAA 1401
QY CAAAAAACCACCGCTACAGCGGTGTTTGTGCGGATCAAGAGTACCACTCTTT 5098
Db 1400 CAAAAAACCACCGCTACAGCGGTGTTTGTGCGGATCAAGAGTACCACTCTTT 1341
QY TTCCGAAGTAACTCGCTTACAGAGCGGATACCAAACTCTCTCTCTAGTGTAGC 5158
Db 1340 TTCCGAAGTAACTCGCTTACAGAGCGGATACCAAACTCTCTCTCTAGTGTAGC 1281
QY CGTAGTTAGGCAACACTTCAAGAACTCTGTAGCAACCGCTTACATACCTCTGCTTAA 5218
Db 1280 CGTAGTTAGGCAACACTTCAAGAACTCTGTAGCAACCGCTTACATACCTCTGCTTAA 1221
QY TCCTGTTACAGTGTCTGCTGAGTGGATGATGATGATGATGATGATGATGATGATGATG 5278
Db 1220 TCCTGTTACAGTGTCTGCTGAGTGGATGATGATGATGATGATGATGATGATGATGATG 1161
QY GACGATAGTTACCGGATAGGCGGAGCGGCTGGGCTGAACGGGGGTTGTCGACACAGC 5338
Db 1160 GACGATAGTTACCGGATAGGCGGAGCGGCTGGGCTGAACGGGGGTTGTCGACACAGC 1101
QY CCAGCTTGAGGGAACGACCTACACGGAATGATGATGATGATGATGATGATGATGATGATG 5398

Db 1100 CCAGCTTGAGCGAAACGACCTACACGAACTGAGATACCTACAGCGTGAGCTATGAGAAA 1041
QY GCSCCAACGCTTCCGGAAGGAGGAAAGCGGACAGGATATCCGGTAAGCGGAGGGTCGGAA 5458
Db 1040 GCSCCAACGCTTCCGGAAGGAGGAAAGCGGACAGGATATCCGGTAAGCGGAGGGTCGGAA 981
QY CAGGAGGCGCACGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTATAGTCTCTCG 5518
Db 980 CAGGAGGCGCACGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTATAGTCTCTCG 921
QY GGTTCGCCACCTCTGACTTGAAGCTGATTTTGTGATGCTGTCAGGGGGGCGGAGCC 5578
Db 920 GGTTCGCCACCTCTGACTTGAAGCTGATTTTGTGATGCTGTCAGGGGGGCGGAGCC 861
QY TATGGAACAAACGCGCAGCAACCGGCTTTTACGGTTCCTGGCTTTTGTGCTGGCTTTG 5638
Db 860 TATGGAACAAACGCGCAGCAACCGGCTTTTACGGTTCCTGGCTTTTGTGCTGGCTTTG 801
QY CTCACATGTTTCTTCTGCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5698
Db 800 CTCACATGTTTCTTCTGCGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
QY AGTGAGCTGATACCGCTCGCGCAGCGCAACCGCAGCGCAGCGCAGCGCAGCGCAGCGAGG 5758
Db 740 AGTGAGCTGATACCGCTCGCGCAGCGCAACCGCAGCGCAGCGCAGCGCAGCGAGG 681
QY AAGCGGAGAGCGCCCAATACGCAACCGCTCTTCCCGCGCGCTTCCCGCGCTTGGCCGATTCA 5818
Db 680 AAGCGGAGAGCGCCCAATACGCAACCGCTCTTCCCGCGCGCTTCCCGCGCTTGGCCGATTCA 621
QY 5819 GCAG 5822
Db 620 GCAG 617

RESULT 4

US-08-675-566-22/c
; Sequence 22, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)									
us-08-675-566-22									
Query Match 43.9%; Score 2553; DB 3; Length 4965;									
Best Local Similarity 97.7%; Pred. No. 0;									
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;									
QY	3134	CCCAATTCGCCCTATAGTAGTGGTATTAACAAATTCACAGCGCGTGGTTTACAAAGTCGT	3193						
DB	4922	CCCAATTCGCCCTATAGTAGTGGTATTAACAAATTCACAGCGCGTGGTTTACAAAGTCGT	4863						
QY	3194	GACTGGGAAACCCCTGGCGTTACCAACTTAATTCGCTTGCAGCACATCCCTTCGCC	3253						
DB	4862	GACTGGGAAACCCCTGGCGTTACCAACTTAATTCGCTTGCAGCACATCCCTTCGCC	4803						
QY	3254	AGCTGGCGTAATAGCAAGAGGCGCCGACCGATTAAGCGCGCTGAGCGGCTGGT	3313						
DB	4802	AGCTGGCGTAATAGCAAGAGGCGCCGACCGATTAAGCGCGCTGAGCGGCTGGT	4743						
QY	3314	AATGGCGAATG-----GACGCGCCCTGTAGCGCGCATTAAGCGCGGCTGGTGGT	3369						
DB	4742	AATGGCGAATGCGCGACGCGCCCTGTAGCGCGCATTAAGCGCGGCTGGTGGT	4683						
QY	3370	ACGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTCGCTTCTTC	3429						
DB	4682	ACGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTCGCTTCTTC	4623						
QY	3430	CCTTCCTTCTCGCCACGTTCCGCGCTTCCGCGCTTCCGCGCTCAAGCTCAAACTCGGGGCTCCCT	3489						
DB	4622	CCTTCCTTCTCGCCACGTTCCGCGCTTCCGCGCTTCCGCGCTCAAGCTCAAACTCGGGGCTCCCT	4563						
QY	3490	TTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGTGAT	3549						
DB	4562	TTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGTGAT	4503						
QY	3550	GGTTACGTAGTGGGCGCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCC	3609						
DB	4502	GGTTACGTAGTGGGCGCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCC	4443						
QY	3610	AGTTCTTTTAAATAGTGGGCTTTGTCGCGCTATTTGTTTAAATAATCAGCTG	3669						
DB	4442	AGTTCTTTTAAATAGTGGGCTTTGTCGCGCTATTTGTTTAAATAATCAGCTG	4383						
QY	3670	TATTCCTTTTATTAAGGGATTTTGGCGATTTCCGCGCTATTTGTTTAAATAATCAGCTG	3729						
DB	4382	TATTCCTTTTATTAAGGGATTTTGGCGATTTCCGCGCTATTTGTTTAAATAATCAGCTG	4323						
QY	3730	ATTTAACAAATTTTAAACCGGAATTTTAAACAAATTTTAAACAAATTTTAAACAAATTTT	3789						
DB	4322	ATTTAACAAATTTTAAACCGGAATTTTAAACAAATTTTAAACAAATTTTAAACAAATTTT	4270						
QY	3790	CGGGTATTTTCTCTTACGCATCTGCGGTATTTTACACCGCATACAGGTGGGCTTTT	3849						
DB	4269	-----CCAGGTGGGCTTTT	4255						
QY	3850	CGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGAT	3909						
DB	4254	CGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGAT	4195						
QY	3910	CCGCTCATGACAAATACCCCTGATAAATGCTTCAATTAATTTGAAAAGGAAGATG	3969						
DB	4194	CCGCTCATGACAAATACCCCTGATAAATGCTTCAATTAATTTGAAAAGGAAGATG	4135						
QY	3970	AGTATTTCAACATTTCCGCTGCGCCCTATTTCCCTTTTGGGCAATTTTGGCTTCTGTT	4029						
DB	4134	AGTATTTCAACATTTCCGCTGCGCCCTATTTCCCTTTTGGGCAATTTTGGCTTCTGTT	4075						
QY	4030	TTTGCTCACCCAGAAACCGCTGTAAGAGTAAAGATGCTGAAGATCAGTTGGGTGACGA	4089						
DB	4074	TTTGCTCACCCAGAAACCGCTGTAAGAGTAAAGATGCTGAAGATCAGTTGGGTGACGA	4015						
QY	4090	GTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGGAA	4149						

5230 GTGGCTGCTCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTA 5289
Db GTGGCTGCTCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTA 2815
QY CCGGATAAGCGGACGCGGTCCGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTCGAG 5349
Db CCGGATAAGCGGACGCGGTCCGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTCGAG 2755
QY CGAACGCTTACACCGAACTGAGTACTCTACAGCGTGAGCTATGAGAAAGCCACGCTT 5409
Db CGAACGCTTACACCGAACTGAGTACTCTACAGCGTGAGCTATGAGAAAGCCACGCTT 2695
QY CCGGAAGGGAGAAAGCGGACAGTATCCGGTAAAGCGGAGCGGGTCCGAAACAGAGAGAGCGC 5469
Db CCGGAAGGGAGAAAGCGGACAGTATCCGGTAAAGCGGAGCGGGTCCGAAACAGAGAGAGCGC 2635
QY ACAGGGAGGCTTCCAGGGGGAAACCGCTTGATCTTTATAGTCTGTGGGTTTCGCGAC 5529
Db ACAGGGAGGCTTCCAGGGGGAAACCGCTTGATCTTTATAGTCTGTGGGTTTCGCGAC 2575
QY CTCTGACTTGAGCGTCAATTTTGTGATCTCTGCTCAGGGGGGCGAGCGCTATGGAAGAAC 5589
Db CTCTGACTTGAGCGTCAATTTTGTGATCTCTGCTCAGGGGGGCGAGCGCTATGGAAGAAC 2515
QY GCCAGCAACGGGCTTTTACGGTTCTGCGCTTTTCTGCGCTTTTGTCTCAATGTTTC 5649
Db GCCAGCAACGGGCTTTTACGGTTCTGCGCTTTTCTGCGCTTTTGTCTCAATGTTTC 2455
QY TTTCTGCTGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTGAGTGAGCTGAT 5709
Db TTTCTGCTGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTGAGTGAGCTGAT 2395
QY ACCGCTGCGGACCGGAAACCGAGCGGAGCGAGTCACTGAGCGAGGAGCGGAGAG 5769
Db ACCGCTGCGGACCGGAAACCGAGCGGAGCGAGTCACTGAGCGAGGAGCGGAGAG 2335
QY CGCCCAATACCAACCGCTCTCCCGCGGTTTGGCGGATTCATTAATGCGAG 5822
Db CGCCCAATACCAACCGCTCTCCCGCGGTTTGGCGGATTCATTAATGCGAG 2282

RESULT 5
US-08-675-566-19/c
; Sequence 19, Application US/08675566
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333

TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-675-566-19

Query Match 43.9%; Score 2553; DB 3; Length 5109;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY 3134 CCCAAATCGCCCTATAGTGTGATGATTAACAATTCATCGCCGTCGTTTACAAACGTCGT 3193
Db 5075 CCCAAATCGCCCTATAGTGTGATGATTAACAATTCATCGCCGTCGTTTACAAACGTCGT 5016
QY 3194 GACTGGGAAACCCCTGCGGTTACCCAACTTAATCGCCTTCGAGCACATCCCCCTTTCGCC 3253
Db 5015 GACTGGGAAACCCCTGCGGTTACCCAACTTAATCGCCTTCGAGCACATCCCCCTTTCGCC 4956
QY 3254 AGCTGGCGTAAATAGCGAAGGCGCCGACCGATCGCCCTTCCCAACAGTTTCGCGAGCTG 3313
Db 4955 AGCTGGCGTAAATAGCGAAGGCGCCGACCGATCGCCCTTCCCAACAGTTTCGCGAGCTG 4896
QY 3314 AATGGCGAATG- ---GACGCGCCCTGTAGCGGCGCATTAAGCGGCGGGGTGTGGTGT 3369
Db 4895 AATGGCGAATGCGCGACGCGCCCTGTAGCGGCGCATTAAGCGGCGGGGTGTGGTGT 4836
QY 3370 ACGGCGAGCTGACGGCTACACTTCCGAGCGCCCTAGCGCGGCTCCCTTCGCTTCTTC 3429
Db 4835 ACGGCGAGCTGACGGCTACACTTCCGAGCGCCCTAGCGCGGCTCCCTTCGCTTCTTC 4776
QY 3430 CTTTCTCTTCGCGCACGTTTCGCGGCTTCCCGCTCAAGCTTAAATCGGGGCTCCCT 3489
Db 4775 CTTTCTCTTCGCGCACGTTTCGCGGCTTCCCGCTCAAGCTTAAATCGGGGCTCCCT 4716
QY 3490 TTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGTGT 3549
Db 4715 TTAGGGTTCCGATTTAGTGTCTTACGGCACCTCGACCGCAAAAACCTTGATTTGGTGT 4656
QY 3550 GGTTCACGTAGTGGCCATCGCCCTGTAGAGGTTTTCGCCCTTCACGCTTGAGTCC 3609
Db 4655 GGTTCACGTAGTGGCCATCGCCCTGTAGAGGTTTTCGCCCTTCACGCTTGAGTCC 4596
QY 3610 ACGTTCTTTAATAGTGGACTCTTGTTCAAAACCTGGAACAACTCAACCTATCTCGGTC 3669
Db 4595 ACGTTCTTTAATAGTGGACTCTTGTTCAAAACCTGGAACAACTCAACCTATCTCGGTC 4536
QY 3670 TATCTTTTGAATTAAGGGAATTTGCGGATTTGCGGCTATTGGTTAAAAATGAGCTG 3729
Db 4535 TATCTTTTGAATTAAGGGAATTTGCGGATTTGCGGCTATTGGTTAAAAATGAGCTG 4476
QY 3730 ATTAAACAAATTTTAAACCGGAAATTTAAACAAATTTAAACGTTTACAAATTTTCGCTGAT 3789
Db 4475 ATTAAACAAATTTTAAACCGGAAATTTAAACAAATTTAAACGTTTACAAATTTTC 4423
QY 3790 GCGGTATTTCTCTTCTAGCATCTGTGCGGTATTTCAACACCGCATACAGCTGGCATT 3849
Db 4422 -----CCAGGTGGCACTTTT 4408
QY 3850 CGGGGAAATGTGCGGGAAACCCCTATTGTTTATTTTCTTAATATCAATTCAAATATGAT 3909
Db 4407 CGGGGAAATGTGCGGGAAACCCCTATTGTTTATTTTCTTAATATCAATTCAAATATGAT 4348
QY 3910 CCGCTCATGAGACAAATACCCCTGATAATGCTTCAATAATTTGAAAAAGGAGATG 3969
Db 4347 CCGCTCATGAGACAAATACCCCTGATAATGCTTCAATAATTTGAAAAAGGAGATG 4288
QY 3970 AGTATTCAAATTTTCGCTGTCGCCCTTATTCCTCTTTTTCGCGCATTTTTCCTGTT 4029
Db 4287 AGTATTCAAATTTTCGCTGTCGCCCTTATTCCTCTTTTTCGCGCATTTTTCCTGTT 4228

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2890
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)840-3333
TELEFAX: (212)840-0712
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6196 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-675-566-5

Query Match 43.9%; Score 2553; DB 3; Length 6196;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;
QY 3134 CCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGCGTCGTTTACAAACGTCGT 3193
DB 6177 CCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGCGTCGTTTACAAACGTCGT 6118
QY 3194 GACTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCCTTGCGAGCACATCCCCCTTTCGCC 3253
DB 6117 GACTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCCTTGCGAGCACATCCCCCTTTCGCC 6058
QY 3254 AGCTGGCGTAATAGCGAAGAGCGCCGACCCGATCGCCCTTCCCAACAGTTGCGGAGCGT 3313
DB 6057 AGCTGGCGTAATAGCGAAGAGCGCCGACCCGATCGCCCTTCCCAACAGTTGCGGAGCGT 5998
QY 3314 AATCGCGAATG---GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGT 3369
DB 5997 AATCGCGAATGCGCGAATGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGT 5938
QY 3370 ACGCGCAGCGTACCGGTACACTTGCACGCGCCCTAGCGCGCGCTCCCTTCGCTTTCCTC 3429
DB 5937 ACGCGCAGCGTACCGGTACACTTGCACGCGCCCTAGCGCGCGCTCCCTTCGCTTTCCTC 5878
QY 3430 CCTTCTCTTTCGCGCAGCTTTCGCGCGCTTTCGCGCTCAAGCTCTAAATCGGGGGTCCCT 3489
DB 5877 CCTTCTCTTTCGCGCAGCTTTCGCGCGCTTTCGCGCTCAAGCTCTAAATCGGGGGTCCCT 5818
QY 3490 TTAGGGTTCGATTTAGAGCTTTAGCGCACTTCGACCGCAAAACCTTGAATTTGGTGTAT 3549
DB 5817 TTAGGGTTCGATTTAGAGCTTTAGCGCACTTCGACCGCAAAACCTTGAATTTAGGTTAT 5758
QY 3550 GGTTCAGCTAGTGGGCCATCGCCCTGTATAGACGGTTCGCGCCCTTTGACGTTGGAGTCC 3609
DB 5757 GGTTCAGCTAGTGGGCCATCGCCCTGTATAGACGGTTCGCGCCCTTTGACGTTGGAGTCC 5698
QY 3610 ACGTCTTTTATAGTGGCTCTTGTTCAAACTGGAAACACCTCAACCCCTATCTCGGTC 3669
DB 5697 ACGTCTTTTATAGTGGCTCTTGTTCAAACTGGAAACACCTCAACCCCTATCTCGGTC 5638
QY 3670 TATCTTTTGTATTTAAGGATTTTTCGCGATTTTCGCGCTATTTGGTTAAAAAATGAGCTG 3729
DB 5637 TATCTTTTGTATTTAAGGATTTTTCGCGATTTTTCGCGCTATTTGGTTAAAAAATGAGCTG 5578
QY 3730 ATTTAACAAATATTAAACGGAATTTTAAACAAATATTAAACGTTTACAAATTTTCGCGTAT 3789
DB 5577 ATTTAACAAATATTAAACGGAATTTTAAACAAATATTAAACGTTTACAAATTTTC----- 5525
QY 3790 GCGGTATTTCTCTTACGCACTCTGCGGTATTTCACACCGCATACAGGTGGCACTTTT 3849
DB 5524 -----CCAGGTGGCACTTTT 5510
QY 3850 CGGGAAATGTGCGGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGAT 3909
DB 5509 CGGGAAATGTGCGGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGAT 5450

QY 3910 CCGCTCATGAGCAATTAACCCCTGATAAATGCTTCAATAATTAATGAAAAAGGAGATATG 3969
DB 5449 CCGCTCATGAGCAATTAACCCCTGATAAATGCTTCAATAATTAATGAAAAAGGAGATATG 5390
QY 3970 AGTATTCAACATTTCCGCTGCGCCTTATCCCTTTTTCGGGCATTTTCCCTTCCCTGTT 4029
DB 5389 AGTATTCAACATTTCCGCTGCGCCTTATTCCTTTTTTTCGGGCATTTTTCCTTCCCTGTT 5330
QY 4030 TTTGCTCACCCAGAAACCGCTGGTGAAGATGCTCAAGATGCTCAAGATCAGTTGGGTGCACGA 4089
DB 5329 TTTGCTCACCCAGAAACCGCTGGTGAAGATGCTCAAGATCAGTTGGGTGCACGA 5270
QY 4090 GTGGTTTACATCGAACTGGATCTCAAACAGCGGTAAAGATCCCTTGAGAGTTTTCGCCCGCAA 4149
DB 5269 GTGGTTTACATCGAACTGGATCTCAAACAGCGGTAAAGATCCCTTGAGAGTTTTCGCCCGCAA 5210
QY 4150 GAAAGTTTCCCAATGATGACACCTTTTAAAGTTCTGCTATGCTGCGCGGTATTTATCCCGT 4209
DB 5209 GAAAGTTTCCCAATGATGACACCTTTTAAAGTTCTGCTATGCTGCGCGGTATTTATCCCGT 5150
QY 4210 ATTGACGCCCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTT 4269
DB 5149 ATTGACGCCCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTT 5090
QY 4270 GAGTACTCACAGTCAAGAAAGCATCTTACCGATGGCATGACAGTAAGAGATTTATGC 4329
DB 5089 GAGTACTCACAGTCAAGAAAGCATCTTACCGATGGCATGACAGTAAGAGATTTATGC 5030
QY 4330 AGTCTGCCATAACCATGATGATAACACTGCGGCCAACTTACTTCTGACAAACGATCGGA 4389
DB 5029 AGTCTGCCATAACCATGATGATAACACTGCGGCCAACTTACTTCTGACAAACGATCGGA 4970
QY 4390 GGAACGGAAGAGCTAAACCGCTTTTTTGCAACAATGCGGGATCATGTAACCTCGCTTGTAT 4449
DB 4969 GGAACGGAAGAGCTAAACCGCTTTTTTGCAACAATGCGGGATCATGTAACCTCGCTTGTAT 4910
QY 4450 CGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCTGACACCAACGATGCT 4509
DB 4909 CGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCTGACACCAACGATGCT 4850
QY 4510 GTAGCAATGCAACAAACGTTGCGCAAACTATTAACTGCGCAAACTTACTTACTTACTAGTCC 4569
DB 4849 GTAGCAATGCAACAAACGTTGCGCAAACTATTAACTGCGCAAACTTACTTACTTACTAGTCC 4790
QY 4570 CGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGGACCACTTCTCGCTCG 4629
DB 4789 CGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGGACCACTTCTCGCTCG 4730
QY 4630 GCCCTTCGCGTGGCTGGTTTATTTGCTGATAAATCTGGAGCCGGTGAGCGTGGTCTCGC 4689
DB 4729 GCCCTTCGCGTGGCTGGTTTATTTGCTGATAAATCTGGAGCCGGTGAGCGTGGTCTCGC 4670
QY 4690 GGTATCATTTGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTATCTAGTATCTATACAG 4749
DB 4669 GGTATCATTTGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTATCTAGTATCTATACAG 4610
QY 4750 ACGGGAGTCAAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTCCTCA 4809
DB 4609 ACGGGAGTCAAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTCCTCA 4550
QY 4810 CTGATTAAAGCAATTTGTTTAAAGGATCTAGTGAAGATCCCTTTTGAATTAATCTCATGACC 4869
DB 4549 CTGATTAAAGCAATTTGTTTAAAGGATCTAGTGAAGATCCCTTTTGAATTAATCTCATGACC 4490
QY 4870 AAACTTCAATTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGAATTAATCTCATGACC 4929
DB 4489 AAACTTCAATTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGAATTAATCTCATGACC 4430
QY 4930 AAAATCCCTTAAACGTTAGTTTTCGTTCCACTGAGCGTCAGACCCCGCTAGAAAGATCAAA 4989
DB 4429 AAAATCCCTTAAACGTTAGTTTTCGTTCCACTGAGCGTCAGACCCCGCTAGAAAGATCAAA 4370
QY 4990 GGAATCTTCTGAGATCCCTTTTTTCTGCGCGTAACTCTGCTGTCACAAACAAAAACCA 5049

Db	4369	GGATCTTCTGAGATCCCTTTTTTCTCGGGTAATCTGCTTGCAGAACAAAAACCA	4310
QY	5050	CCGCTACAGCGGTGGTTGTTCGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTA	5109
Db	4309	CCGCTACAGCGGTGGTTGTTCGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTA	4250
QY	5110	ACTGGCTTCAGACGAGCGAGATACCAAATACTGTCTCTTCTAGTGTAGCGTAGTTAGGC	5169
Db	4249	ACTGGCTTCAGACGAGCGAGATACCAAATACTGTCTCTTCTAGTGTAGCGTAGTTAGGC	4190
QY	5170	CACCACATTCAGAACTCTGTAGCACCGCTACATACTCGCTCTGCTAATCTCTGTACCA	5229
Db	4189	CACCACATTCAGAACTCTGTAGCACCGCTACATACTCGCTCTGCTAATCTCTGTACCA	4130
QY	5230	GTGGCTGTCTGCAGTGGCGATAAGTCTGTCTTACCGGGTTGCACTCAGACGATAGTTA	5289
Db	4129	GTGGCTGTCTGCAGTGGCGATAAGTCTGTCTTACCGGGTTGCACTCAGACGATAGTTA	4070
QY	5290	CCGGATTAAGCGCGACGGTCCGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAG	5349
Db	4069	CCGGATTAAGCGCGACGGTCCGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAG	4010
QY	5350	CGAACGACCTACACCGAACTGAGATACCTACAGGTGAGCTATGAGAAAGCGCCAGCTT	5409
Db	4009	CGAACGACCTACACCGAACTGAGATACCTACAGGTGAGCTATGAGAAAGCGCCAGCTT	3950
QY	5410	CCCGAAGGAGAAAGCGGACAGTATCCGGTAAAGCGGAGGTCGGAACAGGAGAGCGC	5469
Db	3949	CCCGAAGGAGAAAGCGGACAGTATCCGGTAAAGCGGAGGTCGGAACAGGAGAGCGC	3890
QY	5470	ACGAGGAGCTTCCAGGGGAAACGGCTGGTATCTTTATAGTCTCTCGGGTTTCGCCAC	5529
Db	3889	ACGAGGAGCTTCCAGGGGAAACGGCTGGTATCTTTATAGTCTCTCGGGTTTCGCCAC	3830
QY	5530	CTCTGACTTCAGCGTTCGATTTTGTGATGCTCGTACGGGGGCGAGCCCTATGGAAAAAC	5589
Db	3829	CTCTGACTTCAGCGTTCGATTTTGTGATGCTCGTACGGGGGCGAGCCCTATGGAAAAAC	3770
QY	5590	GCACGAAACCGGCCCTTTTACGGTTCCTGGCCCTTTTGTGGCCTTTTGTCTCACATGTTT	5649
Db	3769	GCACGAAACCGGCCCTTTTACGGTTCCTGGCCCTTTTGTGGCCTTTTGTCTCACATGTTT	3710
QY	5650	TTTCTCGCTTATCCCTGATTCGTGGATTAACCGTATTACCGCCTTTTGTGAGTGACTGAT	5709
Db	3709	TTTCTCGCTTATCCCTGATTCGTGGATTAACCGTATTACCGCCTTTTGTGAGTGACTGAT	3650
QY	5710	ACCGCTCGCGACGCGAAACGACCGAGCGACGAGTCAGTGAGCGAGGAACGGAAGAG	5769
Db	3649	ACCGCTCGCGACGCGAAACGACCGAGCGACGAGTCAGTGAGCGAGGAACGGAAGAG	3590
QY	5770	CGCCCAATACGCAAAACCGCTCTCCCGCGCGTTCGCCGATTCATTAATGAG	5822
Db	3589	CGCCCAATACGCAAAACCGCTCTCCCGCGCGTTCGCCGATTCATTAATGAG	3537

RESULT 7
US-08-675-566-14/c
; Sequence 14, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:

/	MEDIUM TYPE:	Floppy disk
/	COMPUTER:	IBM PC compatible
/	OPERATING SYSTEM:	PC-DOS/MS-DOS
/	SOFTWARE:	PatentIn Release #1.0, Version #1.30
/	CURRENT APPLICATION DATA:	
/	APPLICATION NUMBER:	US/08/675,566
/	FILING DATE:	03-JUL-1996
/	CLASSIFICATION:	424
/	ATTORNEY/AGENT INFORMATION:	
/	NAME:	Prommer Esq., William S.
/	REGISTRATION NUMBER:	25,506
/	REFERENCE/DOCKET NUMBER:	454310-2890
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	(212)840-3333
/	TELEFAX:	(212)840-0712
/	INFORMATION FOR SEQ ID NO:	14:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	6243 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
/	MOLECULE TYPE:	DNA (genomic)
/	US-08-675-566-14	
Query Match 43.9%; Score 2553; DB 3; Length 6243;		
Best Local Similarity 97.7%; Pred. No. 0;		
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;		
QY	3134	CCCAATTCGGCCTAATAGTAGTGCATTAACAATCACTGCGCGTGCTTTTACAACTCGT 3193
DB	6224	CCCAATTCGGCCTAATAGTAGTGCATTAACAATCACTGCGCGTGCTTTTACAACTCGT 6165
QY	3194	GACTGGGAACCCCTGGCGTTACCACACTTAATCGCCTTGCAGCACATCCCCCTTTCGCC 3253
DB	6164	GACTGGGAACCCCTGGCGTTACCACACTTAATCGCCTTGCAGCACATCCCCCTTTCGCC 6105
QY	3254	AGCTGGCGTAATAGCGAAGAGGCCGACCGATCGGCCCTTCCAAACAGTTGCGAGCCGTG 3313
DB	6104	AGCTGGCGTAATAGCGAAGAGGCCGACCGATCGGCCCTTCCAAACAGTTGCGAGCCGTG 6045
QY	3314	AATGGCGAATG-----GACGCGCCTCTAGCGCGCATTAAGCGCGCGGTGTGGTGTT 3369
DB	6044	AATGGCGAATGCGCGCACGCGCCTCTAGCGCGCATTAAGCGCGCGGTGTGGTGTT 5985
QY	3370	ACGCGAGCGTAGCCGTACACTTGCAGCGCCTAGCGCGCCTCTTTCGCTTCTTC 3429
DB	5984	ACGCGAGCGTAGCCGTACACTTGCAGCGCCTAGCGCGCCTCTTTCGCTTCTTC 5925
QY	3430	CCTTCCTTTCTCGCCACGTTTCGCGGCTTTCCCGGTCAAAGCTCTAAATCGGGGCTCCCT 3489
DB	5924	CCTTCTTTCTCGCCACGTTTCGCGGCTTTCCCGGTCAAAGCTCTAAATCGGGGCTCCCT 5865
QY	3490	TTAGGTTCCGATTTAGAGCTTTTAGCGCACTTCGACCGCAAAAACTTGATTTGGGTGAT 3549
DB	5864	TTAGGTTCCGATTTAGTGTCTTTTAGCGCACTTCGACCGCAAAAACTTGATTTGGGTGAT 5805
QY	3550	GGTTACAGTAGTGGGCCATCGCCCTGATAGAGCGTTTTTCGCCCTTTCGACGTGAGTCC 3609
DB	5804	GGTTACAGTAGTGGGCCATCGCCCTGATAGAGCGTTTTTCGCCCTTTCGACGTGAGTCC 5745
QY	3610	ACGTTCTTTAATAGTGGACTTTGTTGTCAAAACGGAACAACTCAACCCCTATCTCGTCC 3669
DB	5744	ACGTTCTTTAATAGTGGACTTTGTTGTCAAAACGGAACAACTCAACCCCTATCTCGTCC 5685
QY	3670	TATCTTTTGAATTAAGGGAATTTGCGAATTCGGCTATTTGGTTAAAAAATGAGCTG 3729
DB	5684	TATCTTTTGAATTAAGGGAATTTGCGAATTTGCGAATTTGGTTAAAAAATGAGCTG 5625
QY	3730	ATTTAACAAATATTAACCGCAATTTTAACAAATATTAACCGTTTACAAATTCGCCTGAT 3789
DB	5624	ATTTAACAAATATTAACCGCAATTTTAACAAATATTAACCGTTTACAAATTC----- 5572
QY	3790	GGGTAATTTCTCCTTACGCATCTGTGGGTATTTTCAACACCGCATACAGGTGCGCATTTT 3849

5571 -----CCAGGTGGCACTTTT 5557
Db |||||
QY CGGGAAATGTGCGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGAT 3909
Db |||||
QY CGGGAAATGTGCGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGAT 5497
QY |||||
Db CGGCTCATGACAAATACCCCTGATATAATGCTCAATAATATGAAAGAGAGATG 3969
QY |||||
Db CGGCTCATGACAAATACCCCTGATATAATGCTCAATAATATGAAAGAGAGATG 5437
QY |||||
Db AGTATTCAACATTTCCGCTGTGCGCCCTTATTTCCCTTTTGGGCACTTTTGCCTTCCTGTT 4029
QY |||||
Db AGTATTCAACATTTCCGCTGTGCGCCCTTATTTCCCTTTTGGGCACTTTTGCCTTCCTGTT 5377
QY |||||
Db TTTGCTCACCAGAAACCGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGA 5317
QY |||||
Db GTGGTTTACATCGAACTGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCGGAA 4149
Db |||||
QY GTGGTTTACATCGAACTGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCGGAA 5257
QY |||||
Db GAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGTATGTGGCGCGGTATTTATCCCGT 4209
Db |||||
QY GAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGTATGTGGCGCGGTATTTATCCCGT 5197
QY |||||
Db ATTGACCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTT 5137
QY |||||
Db GAGTACTCACAGTACAGAAAGCATCTTACGATGCGATGACAGTAAGAAATATATGC 4329
QY |||||
Db GAGTACTCACAGTACAGAAAGCATCTTACGATGCGATGACAGTAAGAAATATATGC 5077
QY |||||
Db AGTGTGCGCATTAACCATGATGATTAACATCTGCGGCAACTTACTTCTGACAAACGATCGGA 5017
QY |||||
Db GGACCGAAGGAGCTAACCGCTTTTGTGACAACTGCGGCGGATCATGTAACCTGCTGAT 4449
QY |||||
Db CGTTGCGGAAACCGAGCTGAATGAAGCACTACCAACAGCAGCGTGAACACCAAGATGCT 4509
QY |||||
Db CGTTGCGGAAACCGAGCTGAATGAAGCACTACCAACAGCAGCGTGAACACCAAGATGCT 4897
QY |||||
Db GTAGCAATGGCAACACCGTTGCGCAACTATTAACTGCGCAACTACTTACTAGCTTCC 4569
QY |||||
Db CGGCAACATTAATAGACTGGATGGGCGGATTAAGTTCAGGACCACTTCTGCGCTCG 4629
QY |||||
Db CGGCAACATTAATAGACTGGATGGGCGGATTAAGTTCAGGACCACTTCTGCGCTCG 4777
QY |||||
Db GCGCTTCCGCTGCGTGTATTTGCTGATAATCTGGAGCGGCTGAGCGTGGCTCTCG 4689
QY |||||
Db GCGCTTCCGCTGCGTGTATTTGCTGATAATCTGGAGCGGCTGAGCGTGGCTCTCG 4717
QY |||||
Db GGTATCATGACACTGGGGCGAGATGTAAGCCCTCCCGTATCGTATGTTATCTACAG 4749
QY |||||
Db GGTATCATGACACTGGGGCGAGATGTAAGCCCTCCCGTATCGTATGTTATCTACAG 4657
QY |||||
Db ACGGGAGTCAGCACTATGATGAACCAATAGACAGATCGCTGAGATAGTGTCTCA 4809
Db |||||
QY ACGGGAGTCAGCACTATGATGAACCAATAGACAGATCGCTGAGATAGTGTCTCA 4597
QY |||||
Db CTGATTAGCAATGGTAACTGTGACAGCAAGTTTACTCATATATCTTTAGATTGATTA 4869
Db |||||
QY CTGATTAGCAATGGTAACTGTGACAGCAAGTTTACTCATATATCTTTAGATTGATTA 4537
QY |||||
Db AAACCTCATTTTAAATTAAGGATCTAGGTGAAGATCCTTTTGTATATCTCATGACC 4929

4536 AAACCTCATTTTAAATTAAGGATCTAGGTGAAGATCCTTTTGTATATCTCATGACC 4477
QY |||||
4930 AAACCTCATTTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCGCTAGAAAAGATCAAA 4989
Db |||||
4476 AAACCTCATTTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCGCTAGAAAAGATCAAA 4417
QY |||||
4990 GGATCTTTTGAAGATCCTTTTCTGCGGCTATCTGCTGCTTTCGAAACAAABAACCA 5049
Db |||||
4416 GGATCTTTTGAAGATCCTTTTCTGCGGCTATCTGCTGCTTTCGAAACAAABAACCA 4357
QY |||||
5050 CCGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCACTCTTTTTCGAAAGGTA 5109
Db |||||
4356 CCGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCACTCTTTTTCGAAAGGTA 4297
QY |||||
5110 ACTGGCTTCAGCAGAGCGAGATACCAATACTGCTCTTCTAGTGTAGCCGTAGTTAGC 5169
Db |||||
4296 ACTGGCTTCAGCAGAGCGAGATACCAATACTGCTCTTCTAGTGTAGCCGTAGTTAGC 4237
QY |||||
5170 CACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTTAATCCTGTTACCA 5229
Db |||||
4236 CACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTTAATCCTGTTACCA 4177
QY |||||
5230 GTGGCTGTGCGAGTGGCGATAAGTCTGTCTTACCGGGTTGGAATCAAGACGATGATTA 5289
Db |||||
4176 GTGGCTGTGCGAGTGGCGATAAGTCTGTCTTCTACCGGTTGGAATCAAGACGATGATTA 4117
QY |||||
5290 CCGGATAAGCGCAGCGCTCGGCTGAAACGGGGGTTCGTGCACACAGCCAGCTTGGAG 5349
Db |||||
4116 CCGGATAAGCGCAGCGCTCGGCTGAAACGGGGGTTCGTGCACACAGCCAGCTTGGAG 4057
QY |||||
5350 CGAACGACCTTACACCGAACTGAGATACCTACAGCGTGAAGTATGAAAGCGCCAGCTT 5409
Db |||||
4056 CGAACGACCTTACACCGAACTGAGATACCTACAGCGTGAAGTATGAAAGCGCCAGCTT 3997
QY |||||
5410 CCGGATAAGCGCAGCGCTCGGCTGAAACGGGGGTTCGTGCACACAGCCAGGAGCGC 5469
Db |||||
3996 CCGGATAAGCGCAGCGCTCGGCTGAAACGGGGGTTCGTGCACACAGGAGAGCGC 3937
QY |||||
5470 ACGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTGTGCGGTTTCGCCAC 5529
Db |||||
3936 ACGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTGTGCGGTTTCGCCAC 3877
QY |||||
5530 CTCTGACTGAGCGTGAATTTTGTGATGCTCGTCAGGGGCGGAGCTATGGAAGAAAC 5589
Db |||||
3876 CTCTGACTGAGCGTGAATTTTGTGATGCTCGTCAGGGGCGGAGCTATGGAAGAAAC 3817
QY |||||
5590 GCGCAACAGCGGCTTTTACGGTTCTGCGCTTTTGTGCGCTTTTGTGCTCAGATGTTTC 5649
Db |||||
3816 GCGCAACAGCGGCTTTTACGGTTCTGCGCTTTTGTGCGCTTTTGTGCTCAGATGTTTC 3757
QY |||||
5650 TTTCTGCGTTATCCCTGATTTCTGTGATAAACCGTATTAACCGCTTTTGTGCTCAGATGTTTC 5709
Db |||||
3756 TTTCTGCGTTATCCCTGATTTCTGTGATAAACCGTATTAACCGCTTTTGTGCTCAGATGTTTC 3697
QY |||||
5710 ACCGCTCGCGCAGCGCAACCGAGCGCAGCTGATGAGCGAGCAAGCGGAAGAG 5769
Db |||||
3696 ACCGCTCGCGCAGCGCAACCGAGCGCAGCTGATGAGCGAGCAAGCGGAAGAG 3637
QY |||||
5770 GCGCAACAGCGGCTTTTACGGTTCTGCGCTTTTGTGCGCTTTTGTGCTCAGATGTTTC 5822
Db |||||
3636 GCGCAACAGCGGCTTTTACGGTTCTGCGCTTTTGTGCGCTTTTGTGCTCAGATGTTTC 3584

RESULT 8

US-08-675-566-6/c
; Sequence 6, Application US/08675566
; Patent No. 6090393

GENERAL INFORMATION:

APPLICANT: Fischer, Laurent
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford, P.C.
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/675,566
 FILING DATE: 03-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer Esq., William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2890
 TELEPHONE: (212)840-3333
 TELEFAX: (212)840-0712
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6503 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-675-566-6

Query Match 43.9%; Score 2553; DB 3; Length 6503;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY	3134	CCCAATTCGCCCTATAGTACGATGATTAACAATTCATGSCCGTCGTTTACACGTCGT	3193
Db	6483	CCCAATTCGCCCTATAGTACGATGATTAACAATTCATGSCCGTCGTTTACACGTCGT	6424
QY	3194	GACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCTTGCAGCAATCCCGCTTCGCG	3253
Db	6423	GACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCTTGCAGCAATCCCGCTTCGCG	6364
QY	3254	AGCTGCGCTAATAGCGAAGGAGCGCCGACCGATCGCCCTTCCCAAGTTGCGACGCTG	3313
Db	6363	AGCTGCGCTAATAGCGAAGGAGCGCCGACCGATCGCCCTTCCCAAGTTGCGACGCTG	6304
QY	3314	AATGGCGATG---GACGCGCCCTGTAGCGGCGAATTAAGCGCGCGGTGTGGTGT	3369
Db	6303	AATGGCGAATGCGCGACGCGCCCTGTAGCGGCGAATTAAGCGCGCGGTGTGGTGT	6244
QY	3370	ACGCGACGCTGACCGCTACACTGCGAGCGCCCTAGCGCGCCCTTCCCTTCTTC	3429
Db	6243	ACGCGACGCTGACCGCTACACTGCGAGCGCCCTAGCGCGCCCTTCCCTTCTTC	6184
QY	3430	CCTTCCTTCTCGCCACGTTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	3489
Db	6183	CCTTCCTTCTCGCCACGTTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	6124
QY	3490	TTAGGGTTCCGATTTAGAGCTTTAGCGACCTTCGACCGCAAAAACTTGAGTGGGTGAT	3549
Db	6123	TTAGGGTTCCGATTTAGAGCTTTAGCGACCTTCGACCGCAAAAACTTGAGTGGGTGAT	6064
QY	3550	GGTTACAGTAGTGGGCCATCGCCCTGATAGAGGTTTTCGCCCTTTCACGTTGAGTCC	3609
Db	6063	GGTTACAGTAGTGGGCCATCGCCCTGATAGAGGTTTTCGCCCTTTCACGTTGAGTCC	6004
QY	3610	ACGTTCTTTAATAGTGGACTCTTGTTCAAAACCTGGAACAACACTCAACCTATCTCGGT	3669
Db	6003	ACGTTCTTTAATAGTGGACTCTTGTTCAAAACCTGGAACAACACTCAACCTATCTCGGT	5944
QY	3670	TATCTTTTGTATTAATAGGATTTGCGGCTATTTGGTTAAAAAATGAGCTG	3729

Db	5943	TATCTTTTGTATTAATAGGATTTTCCGGAATTTGGGCTATTTGGTTAAAAAATGAGCTG	5884
QY	3730	ATTTAACAAAATTAATTAACGCGAATTTTAAACAAAATTAATTAACGTTTACAAATTTGCGCTGAT	3789
Db	5883	ATTTAACAAAATTAATTAACGCGAATTTTAAACAAAATTAATTAACGTTTACAAATTTGCGCTGAT	5831
QY	3790	GCGGTATTTCTCCTTAGGATCTGTGGGTATTTTACACCGCATACAGGTGGGACATTTT	3849
Db	5830	-----CCAGGTGGGACATTTT	5816
QY	3850	CGGGAAATGTGCGGAAACCCCTATTTGTTATTTTCTTAAATACATTCAAATATGAT	3909
Db	5815	CGGGAAATGTGCGGAAACCCCTATTTGTTATTTTCTTAAATACATTCAAATATGAT	5756
QY	3910	CCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGAGATG	3969
Db	5755	CCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGAGATG	5696
QY	3970	AGTATTCACATTTCCGTGCGCCCTTATTCCTTTTGGGCAATTTCCCTTCCTGTT	4029
Db	5695	AGTATTCACATTTCCGTGCGCCCTTATTCCTTTTGGGCAATTTCCCTTCCTGTT	5636
QY	4030	TTTGCTCACCCAGAAACGCTGTAAGTAAAGATGCTCAAGATCAGTTGGGTGACGA	4089
Db	5635	TTTGCTCACCCAGAAACGCTGTAAGTAAAGATGCTCAAGATCAGTTGGGTGACGA	5576
QY	4090	GTGGTTACATCGAATGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCGAA	4149
Db	5575	GTGGTTACATCGAATGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCGAA	5516
QY	4150	GAACGTTTCCAAATGATGACACTTTTAAAGTTCTGCTATGTGGCGGTAATTCOCCT	4209
Db	5515	GAACGTTTCCAAATGATGACACTTTTAAAGTTCTGCTATGTGGCGGTAATTCOCCT	5456
QY	4210	ATTGACGCGCGGCAAGCAACTCGGTGCGCGCATACATTTCTCAGAAATGACTTGGTT	4269
Db	5455	ATTGACGCGCGGCAAGCAACTCGGTGCGCGCATACATTTCTCAGAAATGACTTGGTT	5396
QY	4270	GAGTACTACCACTCACAGAAAAGCAATCTTACGATGGATGACATGACATTAAGAAATATGC	4329
Db	5395	GAGTACTACCACTCACAGAAAAGCAATCTTACGATGGATGACATGACATTAAGAAATATGC	5336
QY	4330	AGTGTGCCATTAACATGATGATAACACTGCGGCCAACTTACTTCTGACACGATCGGA	4389
Db	5335	AGTGTGCCATTAACATGATGATAACACTGCGGCCAACTTACTTCTGACACGATCGGA	5276
QY	4390	CGACCAAGAGCTAACCGCTTTTGGACACATGCGGGATCATGTAATCGCCTTGAT	4449
Db	5275	CGACCAAGAGCTAACCGCTTTTGGACACATGCGGGATCATGTAATCGCCTTGAT	5216
QY	4450	CGTTGGGAAACCGAGCTGAATGAAGCCATACCAACACGACGCGGTGACACCGATGCT	4509
Db	5215	CGTTGGGAAACCGAGCTGAATGAAGCCATACCAACACGACGCGGTGACACCGATGCT	5156
QY	4510	GTAGCAATGGCAACAACTTGGCGAAAATTAATTAACGCGCAACTTACTTCTAGCTTC	4569
Db	5155	GTAGCAATGGCAACAACTTGGCGAAAATTAATTAACGCGCAACTTACTTCTAGCTTC	5096
QY	4570	CGGCAACAAATTAATAGACTGAGGCGGATTAAGTTGAGGACCACTTCTGCGCTCG	4629
Db	5095	CGGCAACAAATTAATAGACTGAGGCGGATTAAGTTGAGGACCACTTCTGCGCTCG	5036
QY	4630	GCCCTTCGCGTGGCTGTTTATTTGCTGATAAATCTGGAGCGGTCAGCGGTCTCGC	4689
Db	5035	GCCCTTCGCGTGGCTGTTTATTTGCTGATAAATCTGGAGCGGTCAGCGGTCTCGC	4976
QY	4690	GGTATCATGACGACTGGGCGCAGATGTAAGCCCTCCCGTATCTAGTATTATCTACAG	4749
Db	4975	GGTATCATGACGACTGGGCGCAGATGTAAGCCCTCCCGTATCTAGTATTATCTACAG	4916
QY	4750	ACGGGAGTCAGGCAACTATGGATGAACGAATAAGACATCGCTGAGATAGGTGCTCA	4809
Db	4915	ACGGGAGTCAGGCAACTATGGATGAACGAATAAGACATCGCTGAGATAGGTGCTCA	4856

4810	QY	CTGATTAAAGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATATACTTTAGATTGATTTA	4869
4855	Db	CTGATTAAAGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATATACTTTAGATTGATTTA	4796
4870	QY	AAACTCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATGACC	4929
4795	Db	AAACTCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATGACC	4736
4930	QY	AAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAAGCCCGGTAGAAAAGATCAAA	4989
4735	Db	AAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAAGCCCGGTAGAAAAGATCAAA	4676
4990	QY	GGATCTCTTTGAGATCCCTTTTCTGCGCGTAATCTGCTGTTGCAACCAAAAAACCA	5049
4675	Db	GGATCTCTTTGAGATCCCTTTTCTGCGCGTAATCTGCTGTTGCAACCAAAAAACCA	4616
5050	QY	CCGCTACAGCGGTGGTTTGTTCGCGGATCAAGACTACCAACTCTTTTCCGAAGGTA	5109
4615	Db	CCGCTACAGCGGTGGTTTGTTCGCGGATCAAGACTACCAACTCTTTTCCGAAGGTA	4556
5110	QY	ACTGGCTTCAGCAGAGCGCAGATACCAAAATPACTGTCTCTCTAGTGTAGCGGTAGTGGC	5169
4555	Db	ACTGGCTTCAGCAGAGCGCAGATACCAAAATPACTGTCTCTCTAGTGTAGCGGTAGTGGC	4496
5170	QY	CACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTTACCA	5229
4495	Db	CACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTTACCA	4436
5230	QY	GTGGCTGTCTGCACTGGCGATAAGTCTGTCTTTACCGGGTTGCACTCAAGACGATAGTTA	5289
4435	Db	GTGGCTGTCTGCACTGGCGATAAGTCTGTCTTTACCGGGTTGCACTCAAGACGATAGTTA	4376
5290	QY	CCGATTAAGCGCGCAGCGTTCGGGCTGAAACGGGGGTTCTGTCACACGCGCCTTGGAG	5349
4375	Db	CCGATTAAGCGCGCAGCGTTCGGGCTGAAACGGGGGTTCTGTCACACGCGCCTTGGAG	4316
5350	QY	CGAACGACTACCGAACTCAGATACCTACAGCGTCTGAGCTATGAGAAAGCGCCACGCTT	5409
4315	Db	CGAACGACTACCGAACTCAGATACCTACAGCGTCTGAGCTATGAGAAAGCGCCACGCTT	4256
5410	QY	CCCGAAGGGAAGAAAGCGGACAGGTATCCGGTAAAGCGGCGAGGTTCGGAACAGAGAGCGC	5469
4255	Db	CCCGAAGGGAAGAAAGCGGACAGGTATCCGGTAAAGCGGCGAGGTTCGGAACAGAGAGCGC	4196
5470	QY	ACGAGGGAGCTTCCAGGGGGAAAACGCTGGTATCTTTATAGTCTGTCGCGGTTTCGCCAC	5529
4195	Db	ACGAGGGAGCTTCCAGGGGGAAAACGCTGGTATCTTTATAGTCTGTCGCGGTTTCGCCAC	4136
5530	QY	CTCTCACTTGACGCTCGATTTTGTGATCTCTGCTCAGGGGGCGGAGCCTATCGMAAAC	5589
4135	Db	CTCTCACTTGACGCTCGATTTTGTGATCTCTGCTCAGGGGGCGGAGCCTATCGMAAAC	4076
5590	QY	GCCAGCAAGCGGCTTTTACGGTCTCTGCGCTTTTCTGCGCTTTTGTCTCACTGTC	5649
4075	Db	GCCAGCAAGCGGCTTTTACGGTCTCTGCGCTTTTCTGCGCTTTTGTCTCACTGTC	4016
5650	QY	TTTCTCGGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTGAGTGAAGTGTAT	5709
4015	Db	TTTCTCGGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTGAGTGAAGTGTAT	3956
5710	QY	ACCGCTCGCGCAGCGGACACGACGAGCGCGAGTTCAGTGAGCGAGGACGGAAGAG	5769
3955	Db	ACCGCTCGCGCAGCGGACACGAGCGCGAGTTCAGTGAGCGGAGGACGGAAGAG	3896
5770	QY	CGCCCAATACGAAACCGCTCTCCCGCGGTTGGCCGATTCATTAATGAG	5822
3895	Db	CGCCCAATACGAAACCGCTCTCCCGCGGTTGGCCGATTCATTAATGAG	3843

Patent No. 6090393

GENERAL INFORMATION:

APPLICANT: Fischer, Laurent

TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES, AND METHODS FOR MAKING, AND

TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford, P.C.

STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/675,566

FILING DATE: 03-JUL-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, Esq., William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2890

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)840-3333

TELEFAX: (212)840-0712

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 6958 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

OS-08-675-566-2

Query Match 43.9%; Score 2553; DB 3; Length 6958;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

Qy	3134	CCCAATTCC	CCCTTATAGT	CAGT	CGTATTA	CAATTCA	CTTCACT	CGCGT	CGTTTTT	TACAAC	TCGT	3139				
Db	6938	CCCAATTCC	CCCTTATAGT	CAGT	CGTATTA	CAATTCA	CTTCACT	CGCGT	CGTTTTT	TACAAC	TCGT	6879				
Qy	3194	GACTGG	AAAAA	CCCTCG	CGTTAC	CCCAAC	TTAAT	TCGCTT	CGAC	CAAT	CCCCCTT	TCGCC	3253			
Db	6878	GACTGG	AAAAA	CCCTCG	CGTTAC	CCCAAC	TTAAT	TCGCTT	CGAC	CAAT	CCCCCTT	TCGCC	6819			
Qy	3254	AGTGG	CGTAAT	TAGCG	AAAG	AGGCC	CCAC	CGGAT	CGCCCTT	TCCAA	CAGT	TGCG	CAGCTG	3313		
Db	6818	AGTGG	CGTAAT	TAGCG	AAAG	AGGCC	CCAC	CGGAT	CGCCCTT	TCCAA	CAGT	TGCG	CAGCTG	6759		
Qy	3314	AATGG	CGAATG	---	-CAC	GGCG	CCCTG	TAG	CGG	CGCAT	TAAG	CCG	CGG	CGGTGTGGTGGTT	3369	
Db	6758	AATGG	CGAATG	CGCG	CGCCCT	GATAG	CGG	CGCAT	TAAG	CCG	CGG	CGGTGTGGTGGTT	6699			
Qy	3370	ACGCG	CAGCGT	GAC	CGGTAC	ACTT	TGCG	CAG	CGCCCT	TAG	CGCC	CGCTT	TCGCTT	TCCTC	3429	
Db	6698	ACGCG	CAGCGT	GAC	CGGTAC	ACTT	TGCG	CAG	CGCCCT	TAG	CGCC	CGCTT	TCGCTT	TCCTC	6639	
Qy	3430	CCCTT	CTTTCT	CGC	CAGTTC	CGCG	GGTTT	CCCG	CTTCA	CGCT	CAAG	CTCT	AAAT	CGGG	CGTCCCT	3489
Db	6638	CCCTT	CTTTCT	CGC	CAGTTC	CGCG	GGTTT	CCCG	CTTCA	CGCT	CAAG	CTCT	AAAT	CGGG	CGTCCCT	6579
Qy	3490	TTAGG	GGTTCC	GATTT	TAG	AGCTTT	TAC	GGCA	CCCT	CGAC	CGCA	AAAAA	AACT	TGATTT	GGGTGAT	3549
Db	6578	TTAGG	GGTTCC	GATTT	TAG	AGCTTT	TAC	GGCA	CCCT	CGAC	CGCA	AAAAA	AACT	TGATTT	GGGTGAT	6519
Qy	3550	GGTTC	ACGT	TAGTGG	CCCAT	CGCC	CTGT	TAG	AC	GGTTTTT	CG	CCCTT	TG	CGTTCG	GAGTCC	3609
Db	6518	GGTTC	ACGT	TAGTGG	CCCAT	CGCC	CTGT	TAG	AC	GGTTTTT	CG	CCCTT	TG	CGTTCG	GAGTCC	6459

QY	3610	ACGTTCTTTAATAGTGGACCTCTGTTCCAACTGGAAACACTCAACCCCTATCTCGGTC	3669
Db	6458	ACGTTCTTTAATAGTGGACCTCTGTTCCAACTGGAAACACTCAACCCCTATCTCGGTC	6399
QY	3670	TATTCCTTTGATTTATAAGGATTTTGGCGATTTTCGGCTTATTTGGTTTAAAAATAGAGCTG	3729
Db	6398	TATTCCTTTGATTTATAAGGATTTTGGCGATTTTCGGCTTATTTGGTTTAAAAATAGAGCTG	6339
QY	3730	ATTTAACAATAATTAAACGGATTTTAAACAAATATTAAAGTTTACAAATTCGCGCTGAT	3789
Db	6338	ATTTAACAATAATTAAACGGATTTTAAACAAATATTAAAGTTTACAAATTCGCGCTGAT	6286
QY	3790	GCGGTATTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACACAGTGGCACTTTT	3849
Db	6285	-----CCAGTGGCACTTTT	6271
QY	3850	CGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGTAT	3909
Db	6270	CGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGTAT	6211
QY	3910	CGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGATATG	3969
Db	6210	CGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGATATG	6151
QY	3970	AGTATTCAACATTTCCGCTGTGCGCCCTTATTCCCTTTTTCGGGCAATTTTGCCTTCCTGTT	4029
Db	6150	AGTATTCAACATTTCCGCTGTGCGCCCTTATTCCCTTTTTCGGGCAATTTTGCCTTCCTGTT	6091
QY	4030	TTTGTCCACCGAAGAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGA	4089
Db	6090	TTTGTCCACCGAAGAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGA	6031
QY	4090	GTGGGTATCATCGAATCGATCTCAACAGCGGTAGATCCTTGAGAGTTTTCGCCCGGAA	4149
Db	6030	GTGGGTATCATCGAATCGATCTCAACAGCGGTAGATCCTTGAGAGTTTTCGCCCGGAA	5971
QY	4150	GAAACGTTTTCGAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGTATTTATCCCGT	4209
Db	5970	GAAACGTTTTCGAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGTATTTATCCCGT	5911
QY	4210	ATTGACGCGGCAAGAGCAATCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTT	4269
Db	5910	ATTGACGCGGCAAGAGCAATCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTT	5851
QY	4270	GAGTACTCACCACTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATTATGC	4329
Db	5850	GAGTACTCACCACTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATTATGC	5791
QY	4330	AGTGTGCGATAACCATGAGTGATTAACACTGCGGCCAACTTACTTCTGACACGATCGGA	4389
Db	5790	AGTGTGCGATAACCATGAGTGATTAACACTGCGGCCAACTTACTTCTGACACGATCGGA	5731
QY	4390	GGAACGAAGAGCTAAACCGCTTTTTCACAACTGGGGGATCATGTAACTGCGCTTGAT	4449
Db	5730	GGAACGAAGAGCTAAACCGCTTTTTCACAACTGGGGGATCATGTAACTGCGCTTGAT	5671
QY	4450	CGTTGGGAACCGAGCTGAATGAAGCCATACAAACGACGAGCGGTGAACACAGATGCT	4509
Db	5670	CGTTGGGAACCGAGCTGAATGAAGCCATACAAACGACGAGCGGTGAACACAGATGCT	5611
QY	4510	GTAGCAATGGCAACAACTGTGGCAAACTATTAACTGGCGAATCTTACTTACTAGCTTCC	4569
Db	5610	GTAGCAATGGCAACAACTGTGGCAAACTATTAACTGGCGAATCTTACTTACTAGCTTCC	5551
QY	4570	CGGCAACAATTAACTAGCTGGATGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCG	4629
Db	5550	CGGCAACAATTAACTAGCTGGATGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCG	5491
QY	4630	GCCCTTCGGCTGGCTGTTTATTTGCTGATTAATCTGAGCGCGGTGAGCGTGGGCTCGC	4689
Db	5490	GCCCTTCGGCTGGCTGTTTATTTGCTGATTAATCTGAGCGCGGTGAGCGTGGGCTCGC	5431

QY	4690	GGTATCATTCGACACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAG	4749
Db	5430	GGTATCATTCGACACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAG	5371
QY	4750	ACGGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCA	4809
Db	5370	ACGGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCA	5311
QY	4810	CTGATTAAGCATTTGGTAACTGTCTGAGCAAGTTTACTCATATATATCTTAGATTGATTTA	4869
Db	5310	CTGATTAAGCATTTGGTAACTGTCTGAGCAAGTTTACTCATATATATCTTAGATTGATTTA	5251
QY	4870	AAACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTTGAATATCTCATGACC	4929
Db	5250	AAACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTTGAATATCTCATGACC	5191
QY	4930	AAAAATCCCTTAAAGTGGTTTCTGCTTCCACTGAGCGTCAAGCCCTGAGAAAGATCAAA	4989
Db	5190	AAAAATCCCTTAAAGTGGTTTCTGCTTCCACTGAGCGTCAAGCCCTGAGAAAGATCAAA	5131
QY	4990	GGATCTTCTGAGATCTCTTTTCTGCGGTAAATCTGCTGTGCAAAACAAAAACCA	5049
Db	5130	GGATCTTCTGAGATCTCTTTTCTGCGGTAAATCTGCTGTGCAAAACAAAAACCA	5071
QY	5050	CGCTACCAAGCGGTGGTTTGGTGGCGATCAAGAGTACCACTCTTTTCCGAAAGGTA	5109
Db	5070	CGCTACCAAGCGGTGGTTTGGTGGCGATCAAGAGTACCACTCTTTTCCGAAAGGTA	5011
QY	5110	ACTGGCTTCAGCAGAGCGCAGATACCAATACTGCTCTTCTAGTGPAGCCGTAGTTAGGC	5169
Db	5010	ACTGGCTTCAGCAGAGCGCAGATACCAATACTGCTCTTCTAGTGPAGCCGTAGTTAGGC	4951
QY	5170	CAACAATTCAAGAACTCTGTAGCAACCGCTACATACTCTGCTCTGCTAACTCTGTACCA	5229
Db	4950	CAACAATTCAAGAACTCTGTAGCAACCGCTACATACTCTGCTCTGCTAACTCTGTACCA	4891
QY	5230	GTGGCTGTGCGCAGTGGCGATAGTCTGTCTTACCGGTTGGACTCAAGACGATGTTA	5289
Db	4890	GTGGCTGTGCGCAGTGGCGATAGTCTGTCTTACCGGTTGGACTCAAGACGATGTTA	4831
QY	5290	CCGGATAAGGCGCAGCGTGGGGTGAACGGGGGTTCTGTCACACAGCCCGCTGGAG	5349
Db	4830	CCGGATAAGGCGCAGCGTGGGGTGAACGGGGGTTCTGTCACACAGCCCGCTGGAG	4771
QY	5350	CGAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCCCGCTT	5409
Db	4770	CGAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCCCGCTT	4711
QY	5410	CCGNAAGGAGAAAGGCGGACAGGTATCGGTACGCGGAGGTCGGAAACAGGAGCGC	5469
Db	4710	CCGNAAGGAGAAAGGCGGACAGGTATCGGTACGCGGAGGTCGGAAACAGGAGCGC	4651
QY	5470	ACGAGGAGCTTCCAGGGGGAAACCGCTGTATCTTTATAGTCTGCTGGGTTTCGCCAC	5529
Db	4650	ACGAGGAGCTTCCAGGGGGAAACCGCTGTATCTTTATAGTCTGCTGGGTTTCGCCAC	4591
QY	5530	CTCTGACTTGAGCGTCAATTTTGTGATGCTCGTCAGGGGGCGGAGCTTATGAAAAAC	5589
Db	4590	CTCTGACTTGAGCGTCAATTTTGTGATGCTCGTCAGGGGGCGGAGCTTATGAAAAAC	4531
QY	5590	GCCAGCAACGCGCTTTTACGGTTCTTGCGCTTTTGTGCGCTTTTGTCTCAATGTC	5649
Db	4530	GCCAGCAACGCGCTTTTACGGTTCTTGCGCTTTTGTGCGCTTTTGTCTCAATGTC	4471
QY	5650	TTTCTGCTTATCCCTGATTTCTGTGATAACCGTATTACCGCTTTGAGTGAAGTAT	5709
Db	4470	TTTCTGCTTATCCCTGATTTCTGTGATAACCGTATTACCGCTTTGAGTGAAGTAT	4411
QY	5710	ACCGCTCGCGCAGCGGAAACGACCGAGCGAGTCAAGTGAAGGAGGAGGAGGAG	5769
Db	4410	ACCGCTCGCGCAGCGGAAACGACCGAGCGAGTCAAGTGAAGGAGGAGGAGGAGGAG	4351
QY	5770	CGCCCAATACGCAAAACCGCTCTCTCCCGCGGTTTGGCGGATTCATTAATGACG	5822

Db 4350 CGCCCAATACGAAACCGCTCTCCCGCGGTTGGCCGATTCATTATGACG 4298

RESULT 10
US-08-675-566-13/c
; Sequence 13, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-675-566-13

Query Match 43.9%; Score 2553; DB 3; Length 7379;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY 3134 CCCAATTCGCCCTATAGTAGTCGATTACAAATTCACATGGCGCGTGTTCACAAAGTCGT 3193
Db 4265 CCCAATTCGCCCTATAGTAGTCGATTACAAATTCACATGGCGCGTGTTCACAAAGTCGT 4206

QY 3194 GACTGGGAAACCCCTGGCGTTACCAACTTAATGCGCTTGAGCAGCATCCCCCTTCGCC 3253
Db 4205 GACTGGGAAACCCCTGGCGTTACCAACTTAATGCGCTTGAGCAGCATCCCCCTTCGCC 4146

QY 3254 AGCTGGCGTAATAGCGAAGAGCCCGCAGCCGCTTCCTCCCAACAGTTGGCGAGCCTG 3313
Db 4145 AGCTGGCGTAATAGCGAAGAGCCCGCAGCCGCTTCCTCCCAACAGTTGGCGAGCCTG 4086

QY 3314 AATGGCGAATG---GAGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGT 3369
Db 4085 AATGGCGAATGCGGAGCGGCGCTGTAGCGCGCATTAAGCGCGGTGTGGTGT 4026

QY 3370 ACGCGCAGCGTGAACCGCTACATTGCGAGCGCCCTAGCGCGCGCTTCCTTCCTTC 3429
Db 4025 ACGCGCAGCGTGACCGCTACATTGCGAGCGCCCTAGCGCGCGCTTCCTTCCTTC 3966

QY 3430 CCTTCCTTTCTCGCCACGTTCCCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT 3489
Db 3965 CCTTCCTTTCTCGCCACGTTCCCGCTTTCCTCCCGTCAAGCTCTAAATCGGGGCTCCCT 3906

QY 3490 TTAGGGTTCCGATTTAGAGCTTTACGCACTCGACCGCAAAACTTGATTGGGTGAT 3549
Db 3905 TTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAAAACTTGATTGGGTGAT 3846

QY 3550 GGTTCAGGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACCTTCGAGTCC 3609
Db 3845 GGTTCAGGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACCTTCGAGTCC 3786

QY 3610 ACGTTCTTTAATAGTGGACTCTTTGTTCCAAACTGGAACCAACACTCAACCCCTATTCGGTC 3669
Db 3785 ACGTTCTTTAATAGTGGACTCTTTGTTCCAAACTGGAACCAACACTCAACCCCTATTCGGTC 3726

QY 3670 TATTCCTTTGATTTAAGGATTTTCCGATTTTCGGCTTATTCGGTTAAAAAAGTACGTCG 3729
Db 3725 TATTCCTTTGATTTAAGGATTTTCCGATTTTCCGCTTATTCGGTTAAAAAAGTACGTCG 3666

QY 3730 ATTTAAACAATATTTTACGCGAATTTTAAACAAATATTTAAAGTTTACAAATTCGCTGAT 3789
Db 3665 ATTTAAACAATATTTTACGCGAATTTTAAACAATATTTTAAAGTTTACAAATTCGCTGAT 3613

QY 3790 GCGGTATTTCTCCTTACGCATCTGTGCGGTATTTTCAACCGCATACAGGTGGCACTTTT 3849
Db 3612 -----CCAGGTGGCACTTTT 3598

QY 3850 CGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAATATGTAT 3909
Db 3597 CGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAATATGTAT 3538

QY 3910 CCGCTCATGACAAATACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGAGTATG 3969
Db 3537 CCGCTCATGACAAATACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGAGTATG 3478

QY 3970 AGTATTCAAACATTTCCGTGTCGCCCTTATTTCCCTTTTGTGGCATTTTGTCTCTGTT 4029
Db 3477 AGTATTCAAACATTTCCGTGTCGCCCTTATTTCCCTTTTGTGGCATTTTGTCTCTGTT 3418

QY 4030 TTTGCTACCCAGAAACCGCTGTAAGTAAGTAAGTCTGAGTACAGTTCGGTGCACGA 4089
Db 3417 TTTGCTACCCAGAAACCGCTGTAAGTAAGTCTGAGATCACTGTTGGTGCACGA 3358

QY 4090 GTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCCGAA 4149
Db 3357 GTGGGTTACATCGAATCGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCCGAA 3298

QY 4150 GAAAGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTAATCCCGT 4209
Db 3297 GAAAGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTAATCCCGT 3238

QY 4210 ATTGACGCGGCAAGACAACTCGTTCGCCCATAGACTATTCTCAGAATGACTTGGT 4269
Db 3237 ATTGACGCGGCAAGACAACTCGTTCGCCCATAGACTATTCTCAGAATGACTTGGT 3178

QY 4270 GAGTACTCACAGTACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATATATG 4329
Db 3177 GAGTACTCACAGTACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATATATG 3118

QY 4330 AGTGTGCGCATTAACCATGAGTGAATAACACTCGGCCAACTTACTTCTGACAGATCGGA 4389
Db 3117 AGTGTGCGCATTAACCATGAGTGAATAACACTCGGCCAACTTACTTCTGACAGATCGGA 3058

QY 4390 GAGCGAAGAGCTAACCGCTTTTTCACAACATGGGGGATCATGTAATCGCCTTGAT 4449
Db 3057 GAGCGAAGAGCTAACCGCTTTTTCACAACATGGGGGATCATGTAATCGCCTTGAT 2998

QY 4450 CGTTGGGAAACCGAGCTGAATGAAGCCATACCAACAGCAGCGGTGACACCAAGATGCCT 4509
Db 2997 CGTTGGGAAACCGAGCTGAATGAAGCCATACCAACAGCAGCGGTGACACCAAGATGCCT 2938

QY 4510 GTAGCAATGGCAACAACTGCGGAAACTATTAACTGGGGAACCTACTTACTCTAGCTTCC 4569
Db 2937 GTAGCAATGGCAACAACTGCGGAAACTATTAACTGGGGAACCTACTTACTCTAGCTTCC 2878

QY 4570 CGGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAGGACCACTTCTTCGCTCG 4629

Db 2877 CGGCAAAATTAATAGACTGATGGAGCGGATAAAAGTTTCAGGACCACTTCTCGGCTCG 2818
QY 4630 GCCCTTCCGGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGTCTCGC 4689
Db 2817 GCCCTTCCGGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGTCTCGC 2758
QY 4690 GGTATCATTTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAG 4749
Db 2757 GGTATCATTTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAG 2698
QY 4750 ACGGGAGTCCAGCAACTATGATGATGAACGAATAGACAGATCGCTGAGATAGTGGCTCA 4809
Db 2697 ACGGGAGTCCAGCAACTATGATGATGAACGAATAGACAGATCGCTGAGATAGTGGCTCA 2638
QY 4810 CTGATTAAAGCATTTGTAACCTGTCAGACCAAGTTTACTCATATATCTTTAGATTGATTA 4869
Db 2637 CTGATTAAAGCATTTGTAACCTGTCAGACCAAGTTTACTCATATATCTTTAGATTGATTA 2578
QY 4870 AAACCTTCATTTTAAATTTAAAGGATCTAGTGAAGATCCTTTTGTATATCTCATGACC 4929
Db 2577 AAACCTTCATTTTAAATTTAAAGGATCTAGTGAAGATCCTTTTGTATATCTCATGACC 2518
QY 4930 AAATCCCTTAACGTGAGTTTCTGTTCCACTGAGCGTCAAGCCCGTAGAAAGATCAAA 4989
Db 2517 AAATCCCTTAACGTGAGTTTCTGTTCCACTGAGCGTCAAGCCCGTAGAAAGATCAAA 2458
QY 4990 GGATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTGCTGTCGAAACAAAAACCA 5049
Db 2457 GGATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTGCTGTCGAAACAAAAACCA 2398
QY 5050 CGCTACCAAGCGTGGTGTGTTTTCGCGATCAAGACTCAACACTCTTTTCGAGGTA 5109
Db 2397 CGCTACCAAGCGTGGTGTGTTTTCGCGATCAAGACTCAACACTCTTTTCGAGGTA 2338
QY 5110 ACTGCTTCAGCAGAGCGCAGATACAAATCTGCTCTTCTAGTGTAGCGGTAGTTAGC 5169
Db 2337 ACTGCTTCAGCAGAGCGCAGATACCAATCTGCTCTTCTAGTGTAGCGGTAGTTAGC 2278
QY 5170 CACCACTTCAAGACTCTGAGCAGCGCTATACCGGTGCTGACTCAAGAGATGATTA 5229
Db 2277 CACCACTTCAAGACTCTGAGCAGCGCTATACCGGTGCTGACTCAAGAGATGATTA 2218
QY 5230 GTGGTGTCTGCGGCTGAGTAAAGTCTGCTTACCGGTGCTGACTCAAGAGATGATTA 5289
Db 2217 GTGGTGTCTGCGGCTGAGTAAAGTCTGCTTACCGGTGCTGACTCAAGAGATGATTA 2158
QY 5290 CCGGATAAGCGCAGCGTGGCTGAAACGGGGGTTCGTGCACACAGCCAGCTTGGAG 5349
Db 2157 CCGGATAAGCGCAGCGTGGCTGAAACGGGGGTTCGTGCACACAGCCAGCTTGGAG 2098
QY 5350 CGAAGCACTACACGAACTGAGATACCTACAGCGTGTGATGAGAAAGCGCCAGCTT 5409
Db 2097 CGAAGCACTACACGAACTGAGATACCTACAGCGTGTGATGAGAAAGCGCCAGCTT 2038
QY 5410 CCCGAAGGAGAAAGCGCAGAGTATCGGTAAAGCGGAGGTTCGGAACAGAGAGCGC 5469
Db 2037 CCCGAAGGAGAAAGCGCAGAGTATCGGTAAAGCGGAGGTTCGGAACAGAGAGCGC 1978
QY 5470 ACGAGGAGCTTCCAGGGGAAACCGCTGGTATCTTTATAGTCTGCTGGGTTCGCCAC 5529
Db 1977 ACGAGGAGCTTCCAGGGGAAACCGCTGGTATCTTTATAGTCTGCTGGGTTCGCCAC 1918
QY 5530 CTCACATGAGCTGAGTCTTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAAGAAC 5589
Db 1917 CTCACATGAGCTGAGTCTTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAAGAAC 1858
QY 5590 GCCAGCAACGGGCTTTTACGGTTCTTGGCTTTTGTGCTGCTTTTGTGCTCAGATGTC 5649
Db 1857 GCCAGCAACGGGCTTTTACGGTTCTTGGCTTTTGTGCTGCTTTTGTGCTCAGATGTC 1798
QY 5650 TTTCTGCTTATCCCTGATCTGTGATACCGTATTAACCGCTTTGAGTGTGCTGAT 5709

Db 1797 TTTCTCGCTTATCCCTGATTTCTGTGGATAACCGTATTAACCGCTTTGAGTGAGCTGAT 1738
QY 5710 ACCGCTCGCGCAGCCGAAACGACCGAGCGCAGAGTCACTGAGCGAGGAAGCGGAAGAG 5769
Db 1737 ACCGCTCGCGCAGCCGAAACGACCGAGCGCAGAGTCACTGAGCGAGGAAGCGGAAGAG 1678
QY 5770 CGCCCAATAGCAAAACGGCTCTCCCGCGCGTGGCCGATTCAATTAATGACAG 5822
Db 1677 CGCCCAATAGCAAAACGGCTCTCCCGCGCGTGGCCGATTCAATTAATGACAG 1625

RESULT 11
US-08-675-566-21/c
; Sequence 21, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-675-566-21

Query Match 43.9%; Score 2553; DB 3; Length 8618;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY 3134 CCCAATTCGCCCTATAGTGTAGTGTATTAACAATTCACCTGGCGCTGTTTACCAAGTGT 3193
Db 8598 CCCAATTCGCCCTATAGTGTAGTGTATTAACAATTCACCTGGCGCTGTTTACCAAGTGT 8539
QY 3194 GACTGGGAAACCCCTGGGTTTACCCAACTTAATGCTTGTGAGCAATCCCGCTTTCGCC 3253
Db 8538 GACTGGGAAACCCCTGGGTTTACCCAACTTAATGCTTGTGAGCAATCCCGCTTTCGCC 8479
QY 3254 AGCTGGCGCTATAGCGAAGAGCGCGCACCGATCCCTTCCCAACAGTTGGGAGCTG 3313
Db 8478 AGCTGGCGCTATAGCGAAGAGCGCGCACCGATCCCTTCCCAACAGTTGGGAGCTG 8419
QY 3314 AATGCGCAATG---GACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGT 3369
Db 8418 AATGCGCAATGCGCGACGCGCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGT 8359
QY 3370 ACGCGCAGCTGACGGCTACACTTGGCCAGCGCCCTAGCGCCCTCTCTTCGCTTTCTTC 3429

QY	5590	GCAGCAACGCGCCCTTTTACGGTTCCTGGCCCTTTTGGCTGGCCCTTTTGGCTCAATGTC	5649
Db	6190	GCAGCAACGCGCCCTTTTACGGTTCCTGGCCCTTTTGGCTGGCCCTTTTGGCTCAATGTC	6131
QY	5650	TTTCCTGCGTTATCCCTGATTCCTGTGGATAACCGTATTAACCGCTTTGAGTGAGCTGAT	5709
Db	6130	TTTCCTGCGTTATCCCTGATTCCTGTGGATAACCGTATTAACCGCTTTGAGTGAGCTGAT	6071
QY	5710	ACCGTCGCGCGAGCGCAACGAGCCGAGCGAGTCAGTGACGAGGAGCGAAGAG	5769
Db	6070	ACCGTCGCGCGAGCGCAACGAGCCGAGCGAGTCAGTGACGAGGAGCGAAGAG	6011
QY	5770	CGCCCAATACGCAAAACCGCTCTCCCGCGCGTGGCGGATTAATTAATGAG	5822
Db	6010	CGCCCAATACGCAAAACCGCTCTCCCGCGCGTGGCGGATTAATTAATGAG	5958
RESULT 12			
US-08-675-566-25/c			
; Sequence 25, Application US/08675566			
; Patent No. 6090393			
; GENERAL INFORMATION:			
; APPLICANT: Fischer, Laurent			
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,			
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF			
; NUMBER OF SEQUENCES: 120			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Curtis, Morris & Safford, P.C.			
; STREET: 530 Fifth Avenue			
; CITY: New York			
; STATE: New York			
; COUNTRY: United States of America			
; ZIP: 10036			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/675,566			
; FILING DATE: 03-JUL-1996			
; CLASSIFICATION: 424			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Prommer Esq., William S.			
; REGISTRATION NUMBER: 25,506			
; REFERENCE/DOCKET NUMBER: 454310-2890			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (212)840-3333			
; TELEFAX: (212)840-0712			
; INFORMATION FOR SEQ ID NO: 25:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 8792 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
US-08-675-566-25			
Query Match 43.9%; Score 2553; DB 3; Length 8792;			
Best Local Similarity 97.7%; Pred. No. 0;			
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;			
QY	3134	CCCAATTGCGCCTATAGTAGTTCGTATTACAACTTAATCGCTTGCAGACATCCCCCTTCGCC	3193
Db	8773	CCCAATTGCGCCTATAGTAGTTCGTATTACAACTTAATCGCTTGCAGACATCCCCCTTCGCC	8714
QY	3194	GACTGGGAAAACCCCTGGCGTTACCCAACTTAATCGCTTGCAGACATCCCCCTTCGCC	3253
Db	8713	GACTGGGAAAACCCCTGGCGTTACCCAACTTAATCGCTTGCAGACATCCCCCTTCGCC	8654
QY	3254	AGCTGGCGTAAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGCGAGCGTG	3313

5470 ACAGGAGAGCTTCAGGGGAAACCGCTGGTATCTTTATAGTCTCTGCGGTTTCGCCAC 5529
6485 ACAGGAGAGCTTCAGGGGAAACCGCTGGTATCTTTATAGTCTCTGCGGTTTCGCCAC 6426
5530 CTCTGACTTCAGCGCTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAATAAC 5589
6425 CTCTGACTTCAGCGCTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAATAAC 6366
5590 GCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGTGGCCCTTTTGTCTCATATGTC 5649
6365 GCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGTGGCCCTTTTGTCTCATATGTC 6306
5650 TTTCTGCTTATCCCTGATTCCTGGATTAACCGTATACCGCTTTTGTGAGTCTGAT 5709
6305 TTTCTGCTTATCCCTGATTCCTGGATTAACCGTATACCGCTTTTGTGAGTCTGAT 6246
5710 ACCCTCGCGCAGCCGAAACGACGAGCGAGCGAGTCAGTGAGCGAGAAAGAGAG 5769
6245 ACCCTCGCGCAGCCGAAACGACGAGCGAGCGAGTCAGTGAGCGAGAAAGAGAG 6186
5770 CGCCCAATACGCAACCGCCCTCTCCCGCGGTTGGCCGATCATTAATGAG 5822
6185 CGCCCAATACGCAACCGCCCTCTCCCGCGGTTGGCCGATCATTAATGAG 6133

RESULT 13
US-09-608-730B-21
; Sequence 21, Application US/09608730B
; Patent No. 6423544
; GENERAL INFORMATION:
; APPLICANT: Hardy, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING RECOMBINANT
; TITLE OF INVENTION: VIRIONS
; FILE REFERENCE: PP01569.101
; CURRENT APPLICATION NUMBER: US/09/608,730B
; CURRENT FILING DATE: 2000-06-30
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 4883
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pBS CP
US-09-608-730B-21

Query Match 43.8%; Score 2550; DB 4; Length 4883;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2629; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

3134 CCCAATTCGCCCTATAGTCAGTCGATTAACAATTCATCTGCGCTCGTTTACAACTCGT 3193
1984 CCCAATTCGCCCTATAGTCAGTCGATTAACAATTCATCTGCGCTCGTTTACAACTCGT 2043
3194 GACTGGGAAACCCCTCGCGTTACCCAACTTAATTCGCTTTCGACACATCCCTTCGCC 3253
2044 GACTGGGAAACCCCTCGCGTTACCCAACTTAATTCGCTTTCGACACATCCCTTCGCC 2103
3254 AGTCGCTTAATAGCAAGAGCGCCCGACCGATCGCCCTTCCCAACAGTTGCGAGCGTG 3313
2104 AGTCGCTTAATAGCAAGAGCGCCCGACCGATCGCCCTTCCCAACAGTTGCGAGCGTG 2163
3314 AATGGCGAAT - GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTACG 3372
2164 AATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTACG 2223
3373 CGCAGCGTGAACCGCTACATTTGCGAGCGCCCTAGCGCCCGCTCTTTCGCTTCTCCCT 3432
2224 CGCAGCGTGAACCGCTACATTTGCGAGCGCCCTAGCGCCCGCTCTTTCGCTTCTCCCT 2283
3433 TCCTTTCGCCAGCTTCGCCGCTTTCGCCGCTCAAGCTCTAAATCGCGGCGCTCCCTTTA 3492

4390 GACCGAGAGCTAACCGCTTTTTCGCAACAATGGGGATCATGTAACTCGCTTGAT 4449
7565 GACCGAGAGCTAACCGCTTTTTCGCAACAATGGGGATCATGTAACTCGCTTGAT 7506
4450 CGTTGGCAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGCGCT 4509
7505 CGTTGGCAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGCGCT 7446
4510 GTAGCAATGGCAACCGTTTCGCAACATTAATCTGCGCAACTTAACTTCTAGCTTCC 4569
7445 GTAGCAATGGCAACCGTTTCGCAACATTAATCTGCGCAACTTAACTTCTAGCTTCC 7386
4570 CGGCAACAAATTAATAGACTGAGGAGCGGATTAAGTTGAGGACCACTTCTGCGCTCG 4629
7385 CGGCAACAAATTAATAGACTGAGGAGCGGATTAAGTTGAGGACCACTTCTGCGCTCG 7326
4630 GCCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGGAGCGGTTGAGCGTGGTCTCGC 4689
7325 GCCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGGAGCGGTTGAGCGTGGTCTCGC 7266
4690 GGTATCATGTGAGCACTGGGCGCAGATGGTAAGCCCTCCGATCGTAGTTATCTACAG 4749
7265 GGTATCATGTGAGCACTGGGCGCAGATGGTAAGCCCTCCGATCGTAGTTATCTACAG 7206
4750 ACGGGAGCTCAGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCA 4809
7205 ACGGGAGCTCAGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCA 7146
4810 CTGATTAGCACTTGTAAGTCTGACAGCAAGTTTACTCATATATACTTTAGATTAATTA 4869
7145 CTGATTAGCACTTGTAAGTCTGACAGCAAGTTTACTCATATATACTTTAGATTAATTA 7086
4870 AAACCTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTATTAATCTGAC 4929
7085 AAACCTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTATTAATCTGAC 7026
4930 AAAATCCCTTAAGTGAAGTTTCTGTCACAGCGTCAAGCCCGCTGAGAAAGATCAAA 4989
7025 AAAATCCCTTAAGTGAAGTTTCTGTCACAGCGTCAAGCCCGCTGAGAAAGATCAAA 6966
4990 GATCTCTTGAGATCTTTTTCGCGCTAAATCTGCTGCTGCAAAACAAAACCA 5049
6965 GATCTCTTGAGATCTTTTTCGCGCTAAATCTGCTGCTGCAAAACAAAACCA 6906
5050 CCGCTACCAAGCGGTGTTTTCGCGGATCAAGAGCTACCACTCTTTTCCGAGGTA 5109
6905 CCGCTACCAAGCGGTGTTTTCGCGGATCAAGAGCTACCACTCTTTTCCGAGGTA 6846
5110 ACTGGCTTCAGCAGCGGATACCAAACTACTGCTTCTAGTGTAGCGGTAGTGGC 5169
6845 ACTGGCTTCAGCAGCGGATACCAAACTACTGCTTCTAGTGTAGCGGTAGTGGC 6786
5170 CACCACTTCAAGAACTCTGTAGCAGCGCTTACATCTGCTGCTGCTAAATCTGTTTACCA 5229
6785 CACCACTTCAAGAACTCTGTAGCAGCGCTTACATCTGCTGCTGCTAAATCTGTTTACCA 6726
5230 GTGGCTCTGCGAGTGGCGATAGTGTGTTTACCGGTTGACCTCAAGACATGTTA 5289
6725 GTGGCTCTGCGAGTGGCGATAGTGTGTTTACCGGTTGACCTCAAGACATGTTA 6666
5290 CCGGATAAGCGCAGCGGTGAGCGGGGTTTCGTGCAACAGCCAGCTTGGAG 5349
6665 CCGGATAAGCGCAGCGGTGAGCGGGGTTTCGTGCAACAGCCAGCTTGGAG 6606
5350 CGAACGACCTACACCGAACTGAGTACTTACAGCGTGAAGTATGAGAAAGCGGACGCTT 5409
6605 CGAACGACCTACACCGAACTGAGTACTTACAGCGTGAAGTATGAGAAAGCGGACGCTT 6546
5410 CCGGAAAGGAGGAGCGGATCTCGGTGAGCGGAGGTTGCAACAGGAGAGCGC 5469
6545 CCGGAAAGGAGGAGCGGATCTCGGTGAGCGGAGGTTGCAACAGGAGAGCGC 6486

Db	2284	TCTTTTCTGCGCACGTTTCGCGGCTTTCCCGGTCAAGCTCTAAATCGGGGCTCCCTTTA	2343
QY	3493	GGGTTCCGATTTAGAGCTTTACGGCACCTCGACGCCAAAAAATCTGATTTGGGTGATGGT	3552
Db	2344	GGGTTCCGATTTAGTGTCTTACGGCACCTCGACGCCAAAAAATCTGATTTGGGTGATGGT	2403
QY	3553	TCACGTAGTGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCACG	3612
Db	2404	TCACGTAGTGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCACG	2463
QY	3613	TTCTTTAATAGTGGACTCTGTTCAAACTGGAAACAACACTCAACCCCTATCTCGGCTCAT	3672
Db	2464	TTCTTTAATAGTGGACTCTGTTCAAACTGGAAACAACACTCAACCCCTATCTCGGCTCAT	2523
QY	3673	TCTTTTGATTTAATAGGGAATTTGCGCAATTCGGGCTATTGTTTAAAAAATGAGCTGATT	3732
Db	2524	TCTTTTGATTTAATAGGGAATTTGCGCAATTCGGGCTATTGTTTAAAAAATGAGCTGATT	2583
QY	3733	TAACAAAATATTAAACGGGAATTTTAAACAAAATAATAACGTTTAAACAAATGAGCTGATT	3792
Db	2584	TAACAAAATATTAAACGGGAATTTTAAACAAAATAATAACGTTTAAACAAATGAGCTGATT	2632
QY	3793	GTAATTTCTCCTTAGGCATCTGTGGGTATTTCACCGCATACAGTGGACATTTTCGG	3852
Db	2633	-----AGTGCGCACTTTTCGG	2648
QY	3853	GGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATATCCG	3912
Db	2649	GGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATATCCG	2708
QY	3913	CTCATGAGACATAACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGATATGAGT	3972
Db	2709	CTCATGAGACATAACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGATATGAGT	2768
QY	3973	ATTCAACATTTCCGTGTGCGCCCTATTATCCCTTTTTCGGGCATTTTGCCTTCTGTTTTT	4032
Db	2769	ATTCAACATTTCCGTGTGCGCCCTATTATCCCTTTTTCGGGCATTTTGCCTTCTGTTTTT	2828
QY	4033	GCTCACCCAGAAAACGCTGGTGAAGTAAAAAGATGCTGAAGATCAGTTGGGTGACACAGTG	4092
Db	2829	GCTCACCCAGAAAACGCTGGTGAAGTAAAAAGATGCTGAAGATCAGTTGGGTGACACAGTG	2888
QY	4093	GGTTACATCGAATGGAATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGAAGAA	4152
Db	2889	GGTTACATCGAATGGAATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGAAGAA	2948
QY	4153	CGTTTTCCAATGATGACACTTTTAAAGTCTCGTATGTGGCGCGGTATTATCCCGTATT	4212
Db	2949	CGTTTTCCAATGATGACACTTTTAAAGTCTCGTATGTGGCGCGGTATTATCCCGTATT	3008
QY	4213	GAGCGGGCAAGACAACTCGGTGCGCGCATACATTTCTCAGAATGACTTGGTTGAG	4272
Db	3009	GAGCGGGCAAGACAACTCGGTGCGCGCATACATTTCTCAGAATGACTTGGTTGAG	3068
QY	4273	TACTCACCAGTACAGAAAAGATCTTACGATGGCATGACAGTAAGAGAATTATGAGT	4332
Db	3069	TACTCACCAGTACAGAAAAGATCTTACGATGGCATGACAGTAAGAGAATTATGAGT	3128
QY	4333	GCTGCCATAACCATGATGATAACACTGCGGGCAACTTACTTCTGACACGATCGGAGA	4392
Db	3129	GCTGCCATAACCATGATGATAACACTTGGCGCCAACTTACTTCTGACACGATCGGAGA	3188
QY	4393	CCGAGGAGCTAACCGCTTTTTTGTCAACAATGGGGGATCATGTAACTCGCCTTCATCGT	4452
Db	3189	CCGAGGAGCTAACCGCTTTTTTGTCAACAATGGGGGATCATGTAACTCGCCTTCATCGT	3248
QY	4453	TGGGAACCGAGCTGAATGAGCCATACCAACGACGCGGTGACACCAAGATGCTGTA	4512
Db	3249	TGGGAACCGAGCTGAATGAGCCATACCAACGACGCGGTGACACCAAGATGCTGTA	3308
QY	4513	GCAATGCAACAACGTTGCGCAAACTATTAACTGGGGAACACTTACTACTAGCTTCCGG	4572

QY 5653 CTTGCTTATCCCTGATTTCTGGATAACCGTATTACCGCTTTGAGTGAGCTGATACC 5712
Db 4449 CTTGCTTATCCCTGATTTCTGGATAACCGTATTACCGCTTTGAGTGAGCTGATACC 4508
QY 5713 GCTCGCGCAGCCGAAACGACGAGCGAGCGAGTCACTGAGCGAGGAGCGGAAAGCGC 5772
Db 4509 GCTCGCGCAGCCGAAACGACGAGCGAGCGAGTCACTGAGCGAGGAGCGGAAAGCGC 4568
QY 5773 CCAATACGCAAAACGCTCTCCCGCGGCTTGGCGGATTCATTATATGAG 5822
Db 4569 CCAATACGCAAAACGCTCTCCCGCGGCTTGGCGGATTCATTATATGAG 4618

RESULT 14
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
; GENERAL INFORMATION:
; APPLICANT: Rakhmievich, Alexander
; TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Plinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,206A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 110229.91144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pWRG3169
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1..628
; NAME/KEY: iDNA
; LOCATION: 629..810
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(953..1258, 1332..1673)
; OTHER INFORMATION: /product= "p35 gene product"
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1797..2024
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 2110..2737
; FEATURE:
; NAME/KEY: iDNA

; LOCATION: 2738..2919
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2983..3990
; OTHER INFORMATION: /product= "p40 gene product"
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 4075..4306
; US-08-659-206A-1

Query Match 43.8%; Score 2550; DB 2; Length 7287;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2629; Conservative 0; Mismatches 5; Indels 56; Gaps 2;
QY 3134 CCCAATTGCGCCCTATAGTAGTTCGTATTACAAATTCACATGGCGCTGTTTAAACAGTCTGT 3193
Db 4355 CCCAATTGCGCCCTATAGTAGTTCGTATTACAAATTCACATGGCGCTGTTTAAACAGTCTGT 4414
QY 3194 GACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCTTGCAGACATCCCGCTTTCCG 3253
Db 4415 GACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCTTGCAGACATCCCGCTTTCCG 4474
QY 3254 AGCTGGCGTAAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGCGAGCCTG 3313
Db 4475 AGCTGGCGTAAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGCGAGCCTG 4534
QY 3314 AATGCGGAAT -GGACGCGCCCTGTAGCGCGGATTAAGCGCGGCGGCTGTGCTGTAGG 3372
Db 4535 AATGCGGAATGGACGCGCCCTGTAGCGCGGATTAAGCGCGGCGGCTGTGCTGTAGG 4594
QY 3373 CGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCGCTCTCTTTCGCTTTCCCT 3432
Db 4595 CGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCGCTCTCTTTCGCTTTCCCT 4654
QY 3433 TCCTTTCTCGCCACGTTTCGCGGCTTTCCCGCTTAAGCTCTAAATCGGCGGCTCCCTTTA 3492
Db 4655 TCCTTTCTCGCCACGTTTCGCGGCTTTCCCGCTTAAGCTCTAAATCGGCGGCTCCCTTTA 4714
QY 3493 GGGTTCGGAATTAGAGCTTTACGGACCTCGACCGCAAAACCTTGAATTTGGGTGATGCT 3552
Db 4715 GGGTTCGGAATTAGTGTCTTACGGACCTCGACCGCAAAACCTTGAATTTGGGTGATGCT 4774
QY 3553 TCACGTAGTGGCGCATCGCCCTGATAGAGCGTTTTCGCGCTTTCGACGTTGAGTCCACG 3612
Db 4775 TCACGTAGTGGCGCATCGCCCTGATAGAGCGTTTTCGCGCTTTCGACGTTGAGTCCACG 4834
QY 3613 TTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACAACTCAACCTATCTCGGTCTAT 3672
Db 4835 TTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACAACTCAACCTATCTCGGTCTAT 4894
QY 3673 TCTTTTGAATTATAAGGGATTTTTCGCGATTTTCGCGCTATTTGTTAAATAATGAGCTGATT 3732
Db 4895 TCTTTTGAATTATAAGGGATTTTTCGCGATTTTTCGCGCTATTTGTTAAATAATGAGCTGATT 4954
QY 3733 TAACAAATATTTAAACGGAATTTTAACAAAATATTAACTGTTTACAATTTTCGCGCTGATGCG 3792
Db 4955 TAACAAATATTTAAACGGAATTTTAACAAAATATTAACTGTTTACAATTTTTCGCGCTGATGCG 5003
QY 3793 GTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACAGTGGCACTTTTCGG 3852
Db 5004 -----AGTGGCACTTTTCGG 5019
QY 3853 GGAATGTGCGGGAACCCCTATTTGTTTATTTTCTTAATACATTCATATATGATCCG 3912
Db 5020 GGAATGTGCGGGAACCCCTATTTGTTTATTTTCTTAATAATCATTAATAATGATATCCG 5079
QY 3913 CTCTAGACAAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGAGAGATGAGT 3972
Db 5080 CTCTAGACAAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGAGAGATGAGT 5139
QY 3973 ATTCAACATTTCCGCTGTGCGCTTATTCCTTTTTCGCGCAATTTTCCTCTCTCTTTT 4032
Db 5140 ATTCAACATTTCCGCTGTGCGCTTATTCCTTTTTCGCGCAATTTTCCTCTCTCTTTT 5199

QY 4033 GCTCACCAGAAAACGCTGGTGAAGATGCTGAAGATCAGTTGGGTGCACGAGTG 4092
Db
QY 5200 GCTCACCAGAAAACGCTGGTGAAGATGCTGAAGATCAGTTGGGTGCACGAGTG 5259
Db
QY 4093 GGTATCATCGAACTGAGTCTCAACAGCGGTGAAGATCCTTGAGAGTTTTTCGCCCGAAGAA 4152
Db
QY 5260 GGTATCATCGAACTGAGTCTCAACAGCGGTGAAGATCCTTGAGAGTTTTTCGCCCGAAGAA 5319
Db
QY 4153 CGTTTTCCAAATGATGACGACTTTTAAAGTTCTGCTATGTGGCGGGTATTTATCCCGTATT 4212
Db
QY 5320 CGTTTTCCAAATGATGACGACTTTTAAAGTTCTGCTATGTGGCGGGTATTTATCCCGTATT 5379
Db
QY 4213 GACGCGGGGCAAGACGAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTTGGTTGAG 4272
Db
QY 5380 GACGCGGGGCAAGACGAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTTGGTTGAG 5439
Db
QY 4273 TACTCAGCAGTCAAGAAAAGCATTTTACGGATGGCATGACAGTAAGAGAAATTTATCGAGT 4332
Db
QY 5440 TACTCAGCAGTCAAGAAAAGCATTTTACGGATGGCATGACAGTAAGAGAAATTTATCGAGT 5499
Db
QY 4333 GCTGCCATACCATGATGATACACTGCGGCCAACTTACTTCTGACAAAGATCGGAGGA 4392
Db
QY 5500 GCTGCCATACCATGATGATACACTGCGGCCAACTTACTTCTGACAAAGATCGGAGGA 5559
Db
QY 4393 CCGAAGGAGCTAACCGGTTTTTGCACAAATGCGGGGATCATGTAACTCGSCCTTGATCGT 4452
Db
QY 5560 CCGAAGGAGCTAACCGGTTTTTGCACAAATGCGGGGATCATGTAACTCGSCCTTGATCGT 5619
Db
QY 4453 TGGGAACCGGAGTGAATGAAGCCATACCAAACGAGCGGTGACACCAACGATGCGCTGTA 4512
Db
QY 5620 TGGGAACCGGAGTGAATGAAGCCATACCAAACGAGCGGTGACACCAACGATGCGCTGTA 5679
Db
QY 4513 GCAATGCGCAACACGTTGGCGAACTTAACTGGCGAACTACTTACTCTAGTCTCCCGG 4572
Db
QY 5680 GCAATGCGCAACACGTTGGCGAACTTAACTGGCGAACTACTTACTCTAGTCTCCCGG 5739
Db
QY 4573 CAACAATTAATAGACTGGATGAGCGGATAAAGTTGCGAGGACCACTCTCGCTCGGCG 4632
Db
QY 5740 CAACAATTAATAGACTGGATGAGCGGATAAAGTTGCGAGGACCACTCTCGCTCGGCG 5799
Db
QY 4633 CTTCCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCGCGGTGAGCGTGGCTCGCGGT 4692
Db
QY 5800 CTTCCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCGCGGTGAGCGTGGCTCGCGGT 5859
Db
QY 4693 ATCATTGACGACTGCGGCGAGTGTAGCCCTCCCGTATCGTAGTTATCTACAGCAG 4752
Db
QY 5860 ATCATTGACGACTGCGGCGAGTGTAGCCCTCCCGTATCGTAGTTATCTACAGCAG 5919
Db
QY 4753 GGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCAGTG 4812
Db
QY 5920 GGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCAGTG 5979
Db
QY 4813 ATTAAGATTTGATATGTCAGCAAGTTTACTCATATATCTTTAGATTGATTAAAA 4872
Db
QY 5980 ATTAAGATTTGATATGTCAGCAAGTTTACTCATATATCTTTAGATTGATTAAAA 6039
Db
QY 4873 CTTTATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTATTAATCTCATGACCAA 4932
Db
QY 6040 CTTTATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTATTAATCTCATGACCAA 6099
Db
QY 4933 ATCCCTTAACTGAGTTTCTGCTTCCACTGAGCGGTGAGACCCGCTAGAAAGATCAAGA 4992
Db
QY 6100 ATCCCTTAACTGAGTTTCTGCTTCCACTGAGCGGTGAGACCCGCTAGAAAGATCAAGA 6159
Db
QY 4993 TCTTCTGAGATCTCTTTTCTGCGCGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5052
Db
QY 6160 TCTTCTGAGATCTCTTTTCTGCGCGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6219
Db
QY 5053 CTACAGCGGTGGTTGTTGGCGGATCAAGAGTACCAACTCTTTTTCGGAAGTAACT 5112
Db
QY 6220 CTACAGCGGTGGTTGTTGGCGGATCAAGAGTACCAACTCTTTTTCGGAAGTAACT 6279

QY 5113 GGCTTCAGCAGAGCGCAGATACCAAAATACCTGCTCTTCTAGTGTAGCCGTAGTTAGGCCAC 5172
Db
QY 6280 GGCTTCAGCAGAGCGCAGATACCAAAATACCTGCTCTTCTAGTGTAGCCGTAGTTAGGCCAC 6339
Db
QY 5173 CACTTCAAGAACTCTGTAGCAGCGCTACATACCTGCTCTGCTTAATCTGTTTACCAAGTG 5232
Db
QY 6340 CACTTCAAGAACTCTGTAGCAGCGCTACATACCTGCTCTGCTTAATCTGTTTACCAAGTG 6399
Db
QY 5233 GCTGCTCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG 5292
Db
QY 6400 GCTGCTCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG 6459
Db
QY 5293 GATAAGCGCGCAGCGCTCGGCTGAAACGGGGGTTCTGTGACACAGCCAGCTTGGAGCGA 5352
Db
QY 6460 GATAAGCGCGCAGCGCTCGGCTGAAACGGGGGTTCTGTGACACAGCCAGCTTGGAGCGA 6519
Db
QY 5353 ACCACCTTACACCGAACTTGAGATACCTACAGCGGTGAGCTAGAGAAAGCGGACCTTCCC 5412
Db
QY 6520 ACCACCTTACACCGAACTTGAGATACCTACAGCGGTGAGCTAGAGAAAGCGGACCTTCCC 6579
Db
QY 5413 GAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGTCGGAACAGGAGAGCGCACG 5472
Db
QY 6580 GAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGTCGGAACAGGAGAGCGCACG 6639
Db
QY 5473 AGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCTCTGCGGTTTCGCCACTC 5532
Db
QY 6640 AGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCTCTGCGGTTTCGCCACTC 6699
Db
QY 5533 TGACTTGAGCGTCAATTTTGTGATCTCTGTCAGGGGCGGAGCTTATGTAAGAAAGCGC 5592
Db
QY 6700 TGACTTGAGCGTCAATTTTGTGATCTCTGTCAGGGGCGGAGCTTATGTAAGAAAGCGC 6759
Db
QY 5593 AGCAACGCGGCTTTTACGGTTCTTGGCTTTTGTGCTTGTGCTCAGATGTTCTTT 5652
Db
QY 6760 AGCAACGCGGCTTTTACGGTTCTTGGCTTTTGTGCTTGTGCTCAGATGTTCTTT 6819
Db
QY 5653 CTTGCGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTGAGTGAGCTGATACC 5712
Db
QY 6820 CTTGCGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTGAGTGAGCTGATACC 6879
Db
QY 5713 GTCGCGCGCAGCGCAACGACCGCGCAGCGAGTCACTGAGCGAGAAAGCGGAGAGCGC 5772
Db
QY 6880 GTCGCGCGCAGCGCAACGACCGCGAGCGAGTCACTGAGCGAGAAAGCGGAGAGCGC 6939
Db
QY 5773 CCAATACGCAACCGCTCTCCCGCGCTTCCCGGCTTCAATTAATGACG 5822
Db
QY 6940 CCAATACGCAACCGCTCTCCCGCGCTTCCCGGCTTCAATTAATGACG 5989

RESULT 15

US-08-472-809B-7/c
; Sequence 7, Application US/08472809B
; Patent No. 5925564
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: DeMayo, Franco J.
; APPLICANT: O'Malley, Bert W.
; TITLE OF INVENTION: Expression Vector Systems and
; TITLE OF INVENTION: Method of Use
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: US/08/472.809B
APPLICATION NUMBER: 08/209.846
FILING DATE: June 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209.846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789.919
FILING DATE: No. 592564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6345 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-08-472-809B-7

Query Match 43.8%; Score 2549; DB 2; Length 6345;
Beat Local Similarity 97.7%; Pred. No. 0;
Matches 2628; Conservative 0; Mismatches 5; Indels 56; Gaps 2;
QY 3135 CCAATTCGCCCTATAGTGGTACCTTAAATCGGCTTGACGACATCCCTTTGCGCA 3194
DB 2892 CCAATTCGCCCTATAGTGGTACCTTAAATCGGCTTGACGACATCCCTTTGCGCA 2833
QY 3195 ACTGGGAAACCCCTGGCGTTACCCAACTTAAATCGGCTTGACGACATCCCTTTGCGCA 3254
DB 2832 ACTGGGAAACCCCTGGCGTTACCCAACTTAAATCGGCTTGACGACATCCCTTTGCGCA 2773
QY 3255 GTCGGGTAAATAGCGAAGGCGCGACGATCGCCCTTCCCAAGTTGCGCGCTGA 3314
DB 2772 GCTGGCGTAAATAGCGAAGGCGCGACGATCGCCCTTCCCAAGTTGCGCGCTGA 2713
QY 3315 ATGGCGAAT-GGACGGCCCTGTAGCGGCGCATTAAGCGCGCGGTGTGGTTACGC 3373
DB 2712 ATGGCGAATGGACGGCCCTGTAGCGGCGCATTAAGCGCGCGGTGTGGTTACGC 2653
QY 3374 GCAGCGTACCGCTACACTTGCAGCGCCCTAGCGCCGCTCTTTTCCCTTT 3433
DB 2652 GCAGCGTACCGCTACACTTGCAGCGCCCTAGCGCCGCTCTTTTCCCTTT 2593
QY 3434 CCTTCTCGCAGTTTCGGGCTTCCCGTCAAGCTCTAATCGGGGCTCCCTTTAG 3493
DB 2592 CCTTCTCGCAGTTTCGGGCTTCCCGTCAAGCTCTAATCGGGGCTCCCTTTAG 2533
QY 3494 GGTTCGATTTAGAGCTTTACGCACTTCGACCGCAAAAACCTTGATTTGGGTGATGGTT 3553
DB 2532 GGTTCGATTTAGAGCTTTACGCACTTCGACCGCAAAAACCTTGATTTAGGTTGATGGTT 2473
QY 3554 CAGCTAGTGGGCAATCGCCCTGATAGAGGTTTTTTCGGCTTTTGAAGTGGAGTCCAGCT 3613
DB 2472 CAGCTAGTGGGCAATCGCCCTGATAGAGGTTTTTTCGGCTTTTGAAGTGGAGTCCAGCT 2413
QY 3614 TCCTTAATAGTGACCTTTGTTCCAACTGGAAACACACTCAACCTTATCTCGGTCTATT 3673
DB 2412 TCCTTAATAGTGACCTTTGTTCCAACTGGAAACACACTCAACCTTATCTCGGTCTATT 2353
QY 3674 CTTTTCGATTTAAGGGAATTTTCCGCTATTCGGCTATTTGGTTAAAAAATGAGCTGATT 3733
DB 2352 CTTTTCGATTTAAGGGAATTTTCCGCTATTTCCGCTATTTGGTTAAAAAATGAGCTGATT 2293
QY 3734 ACAAATATTTAAGCGGAATTTTAAACAAATATTTAAGCTTTACATTTCCCTGATCGCG 3793

DB 2292 AACAAAATTTAAGCGGAATTTTAAACAAATATTTAAGCTTTACAAATTT----- 2245
QY 3794 TATTTTCTCTTACGCATCTGTGCGGTATTTTCAACCGCATACAGGTGGGCACTTTTCGGG 3853
DB 2244 -----AGGTGGCACTTTTCGGG 2228
QY 3854 GAAATGTGCGGGAACCCCTATTTTGTATTTTCTAAATACATTTCAATATGTATCGC 3913
DB 2227 GAAATGTGCGGGAACCCCTATTTTGTATTTTCTAAATACATTTCAATATGTATCGC 2168
QY 3914 TCATGAGACAAATAACCCCTGATAATGCTTCAATAATTTGAAAAGGAAGATGAGTA 3973
DB 2167 TCATGAGACAAATAACCCCTGATAATGCTTCAATAATTTGAAAAGGAAGATGAGTA 2108
QY 3974 TTCAACATTTCCGTGTGCGCCCTTATTCCTTTTGTGGGCAATTTTGCCTTCTGTTTGG 4033
DB 2107 TTCAACATTTCCGTGTGCGCCCTTATTCCTTTTGTGGGCAATTTTGCCTTCTGTTTGG 2048
QY 4034 CTCACCCGAAAACCGTGTGTAAGATGCTGAAGATCAGTTGGTGCACAGTGG 4093
DB 2047 CTCACCCGAAAACCGTGTGTAAGATGCTGAAGATCAGTTGGTGCACAGTGG 1988
QY 4094 GTTACATCGAACTGGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAAGAC 4153
DB 1987 GTTACATCGAACTGGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAAGAC 1928
QY 4154 GTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTTATCCCTGATTG 4213
DB 1927 GTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTTATCCCTGATTG 1868
QY 4214 AGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACITGGTTGAGT 4273
DB 1867 AGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACITGGTTGAGT 1808
QY 4274 ACTCACAGTACAGAAAGCATCTTACGGATGCGATGACAGTAAGAGAAATTTATCGAGTG 4333
DB 1807 ACTCACAGTACAGAAAGCATCTTACGGATGCGATGACAGTAAGAGAAATTTATCGAGTG 1748
QY 4334 CTGCCATAACCATGATGATGATAACACTTTCGCGGCGCAACTTCTGCAACAGTTCGGAGGAC 4393
DB 1747 CTGCCATAACCATGATGATGATAACACTTTCGCGGCGCAACTTCTGCAACAGTTCGGAGGAC 1688
QY 4394 CGAAGGAGTAAACCGCTTTTTCGCAACATGGGGATCATGTAATCTGCTGCTGATCGTT 4453
DB 1687 CGAAGGAGTAAACCGCTTTTTCGCAACATGGGGATCATGTAATCTGCTGCTGATCGTT 1628
QY 4454 GCGAACCAGGAGCTGATGAAAGCATACCAACAGAGCGTGACCAACGATGCTGCTGATG 4513
DB 1627 GCGAACCAGGAGCTGATGAAAGCATACCAACAGAGCGTGACCAACGATGCTGCTGATG 1568
QY 4514 CAATGCGCAACACGTTGCGCAAACTTATTAATCTGGCGCACTACTTACTCTAGCTTCCCGGC 4573
DB 1567 CAATGCGCAACACGTTGCGCAAACTTATTAATCTGGCGCACTACTTACTCTAGCTTCCCGGC 1508
QY 4574 AACAAATATGACTGGATGGAGGGGATAAAGTTTCAGACCACTTCTGCGCTCGCGCC 4633
DB 1507 AACAAATATGACTGGATGGAGGGGATAAAGTTTCAGACCACTTCTGCGCTCGCGCC 1448
QY 4634 TTCCCGCTCGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTA 4693
DB 1447 TTCCCGCTCGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTA 1388
QY 4694 TCATTCAGCACTGGGGCCAGATGGTAAAGCTTCCGCTATCTAGTATCTACACGACGG 4753
DB 1387 TCATTCAGCACTGGGGCCAGATGGTAAAGCTTCCGCTATCTAGTATCTACACGACGG 1328
QY 4754 GGAGTCAGCACTATGAGTGAACGAAATAGACAGATCGCTGAGATAGTGGTGCCTCACTGA 4813
DB 1327 GGAGTCAGCACTATGAGTGAACGAAATAGACAGATCGCTGAGATAGTGGTGCCTCACTGA 1268
QY 4814 TTAAGCAATTTGGTAACCTGTGAGCAACAGTTTACTCATATATCTTTAGATTTGATTTAAAC 4873
DB 1267 TTAAGCAATTTGGTAACCTGTGAGCAACAGTTTACTCATATATCTTTAGATTTGATTTAAAC 1208

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 14:36:08 ; Search time 1542 Seconds
(without alignments)

17296.434 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagcagcaggttcccg.....tggcagcattcaatgacg 5822

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	5822	100.0	5822	13 US-09-924-197-1
2	2768	47.5	4773	10 US-09-991-209-32
3	2768	47.5	4950	10 US-09-991-209-34
4	2768	47.5	4965	10 US-09-991-209-37
5	2768	47.5	4974	10 US-09-991-209-35
6	2768	47.5	5001	10 US-09-991-209-40
7	2768	47.5	5034	10 US-09-991-209-33
8	2768	47.5	5164	10 US-09-991-209-36
9	2768	47.5	5277	10 US-09-991-209-25
10	2768	47.5	5295	10 US-09-991-209-38
11	2768	47.5	5327	10 US-09-991-209-27
12	2768	47.5	5337	10 US-09-991-209-19
13	2768	47.5	5337	10 US-09-991-209-23
14	2768	47.5	5337	10 US-09-991-209-31

15	2768	47.5	5338	10	US-09-991-209-15	Sequence 15, Appl
16	2768	47.5	5338	10	US-09-991-209-29	Sequence 29, Appl
17	2768	47.5	5345	10	US-09-991-209-17	Sequence 17, Appl
18	2768	47.5	5387	10	US-09-991-209-41	Sequence 41, Appl
19	2768	47.5	5395	10	US-09-991-209-21	Sequence 21, Appl
20	2683.4	46.1	3448	15	US-10-128-590-6	Sequence 6, Appl
21	2683.4	46.1	3448	15	US-10-128-587A-6	Sequence 6, Appl
22	2683.4	46.1	3448	15	US-10-128-578B-6	Sequence 6, Appl
23	2675.4	46.0	3018	13	US-09-486-142-7	Sequence 7, Appl
24	2670.2	45.9	3357	15	US-10-161-403-96	Sequence 96, Appl
25	2552	43.8	10078	14	US-10-033-190-3	Sequence 3, Appl
26	2549.4	43.8	2962	15	US-10-033-399B-10	Sequence 10, Appl
27	2549.4	43.8	3057	15	US-10-033-399B-23	Sequence 23, Appl
28	2549.4	43.8	3093	15	US-10-033-399B-7	Sequence 7, Appl
29	2549.4	43.8	5251	14	US-10-153-159-17	Sequence 17, Appl
30	2549.4	43.8	5251	15	US-10-153-176-17	Sequence 17, Appl
31	2549.4	43.8	5251	16	US-10-443-134A-17	Sequence 17, Appl
32	2549	43.8	2958	15	US-10-220-262-2	Sequence 2, Appl
33	2549	43.8	2958	15	US-10-220-262-3	Sequence 3, Appl
34	2549	43.8	2958	15	US-10-220-262-4	Sequence 4, Appl
35	2549	43.8	3351	16	US-10-014-099F-72	Sequence 72, Appl
36	2549	43.8	4754	16	US-10-014-099F-80	Sequence 80, Appl
37	2549	43.8	4773	16	US-10-014-099F-81	Sequence 81, Appl
38	2549	43.8	4831	16	US-10-014-099F-99	Sequence 99, Appl
39	2548.8	43.8	8858	15	US-10-378-393-1	Sequence 1, Appl
40	2538.2	43.6	10597	15	US-10-057-108-10	Sequence 10, Appl
41	2538.2	43.6	10599	15	US-10-057-108-11	Sequence 11, Appl
42	2538.2	43.6	12482	15	US-10-057-108-7	Sequence 7, Appl
43	2531.2	43.5	5175	15	US-10-057-108-6	Sequence 6, Appl
44	2531.2	43.5	8426	15	US-10-163-899-1	Sequence 1, Appl
45	2515	43.2	13910	10	US-09-919-901-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-924-197-1
; Sequence 1, Application US/09924197
; Publication No. US20030018993A1
; GENERAL INFORMATION:
; APPLICANT: Gutterson, Neal
; APPLICANT: Oeller, Paul
; TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted
; TITLE OF INVENTION: Repeat Sequences
; FILE REFERENCE: 012176-010810US
; CURRENT APPLICATION NUMBER: US/09/924,197
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/225,508
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-924-197-1

Query Match	100.0%	Score 5822;	DB 13;	Length 5822;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5822;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTGCGACGACAGGTTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAG	60	
Db	1	CTGCGACGACAGGTTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAG	60	
Qy	61	TTAGTCACTCAATTAGGACCCCGAGTTTACACTTTTATGCTTCGGCTCGTATGTTGTG	120	
Db	61	TTAGTCACTCAATTAGGACCCCGAGTTTACACTTTTATGCTTCGGCTCGTATGTTGTG	120	
Qy	121	TGGAAATGTGACGGGATAACAAATTTACACAGGAAACAGCTATGACCATGATTCAGCGCAA	180	
Db	121	TGGAAATGTGACGGGATAACAAATTTACACAGGAAACAGCTATGACCATGATTCAGCGCAA	180	

QY 4561 CTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTTGACGACCACTT 4620
Db 4561 CTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTTGACGACCACTT 4620
QY 4621 CTGGCTCGGCGCTTCCGGCTGGCTGGTTTATTTCTGTATTAATCTGGAGCGGTTGAGCGT 4680
Db 4621 CTGGCTCGGCGCTTCCGGCTGGCTGGTTTATTTCTGTATTAATCTGGAGCGGTTGAGCGT 4680
QY 4681 GGGTCTCGCGGTATCATATGACGACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT 4740
Db 4681 GGGTCTCGCGGTATCATATGACGACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT 4740
QY 4741 ATCTACAGCGGGGAGTCAAGCACTATGATGAACGAAATAGACAGATCGCTGAGATA 4800
Db 4741 ATCTACAGCGGGGAGTCAAGCACTATGATGAACGAAATAGACAGATCGCTGAGATA 4800
QY 4801 GGTGCTCACTGATTAAAGCATTTGGTAAGTCTGACACCAAGTTTACTCATATATATTTAG 4860
Db 4801 GGTGCTCACTGATTAAAGCATTTGGTAAGTCTGACACCAAGTTTACTCATATATATTTAG 4860
QY 4861 ATTGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAAT 4920
Db 4861 ATTGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAAT 4920
QY 4921 CTCATGACCAAAATCCCTTAACGCTGAGTTTTCCTTCCACTGAGCGCTGACACCCCGTAGAA 4980
Db 4921 CTCATGACCAAAATCCCTTAACGCTGAGTTTTCCTTCCACTGAGCGCTGACACCCCGTAGAA 4980
QY 4981 AAGATCAAAAGGATCTTCTTGAGATCCTTTTTCCTGCGGTAAATCTGCTGCTGCAAAACA 5040
Db 4981 AAGATCAAAAGGATCTTCTTGAGATCCTTTTTCCTGCGGTAAATCTGCTGCTGCAAAACA 5040
QY 5041 AAAAAACCAACCGCTACAGCGGTGGTTTGTTCGGGATCAAGACTACCAACTCTTTT 5100
Db 5041 AAAAAACCAACCGCTACAGCGGTGGTTTGTTCGGGATCAAGACTACCAACTCTTTT 5100
QY 5101 CGAAGGTAACCTGGCTTACAGCAGCGCAGATACCAATACCTCTCTAGTAGCGG 5160
Db 5101 CGAAGGTAACCTGGCTTACAGCAGCGCAGATACCAATACCTCTCTAGTAGCGG 5160
QY 5161 TAGTTAGGCGCACCTTCAAGAACTCTGTAGCACCGCCTACATACCTGCTCTGTAATC 5220
Db 5161 TAGTTAGGCGCACCTTCAAGAACTCTGTAGCACCGCCTACATACCTGCTCTGTAATC 5220
QY 5221 CTGTTACAGTGGCTCTGCTGAGTGGCGATAGTCTGTCTTACCGGGTGGACTCAAGA 5280
Db 5221 CTGTTACAGTGGCTCTGCTGAGTGGCGATAGTCTGTCTTACCGGGTGGACTCAAGA 5280
QY 5281 CGATAGTTACCGGATAGCGCGAGCGGTCTGGGCTGAACGGGGGTTCTGTGACACAGCC 5340
Db 5281 CGATAGTTACCGGATAGCGCGAGCGGTCTGGGCTGAACGGGGGTTCTGTGACACAGCC 5340
QY 5341 AGCTTGAGCGAAACGACCTACACCGAACTGAGATACCTAAGCGTGAAGTATGAGAAGC 5400
Db 5341 AGCTTGAGCGAAACGACCTACACCGAACTGAGATACCTAAGCGTGAAGTATGAGAAGC 5400
QY 5401 GCCACGCTTCCGAAAGGAGAAAGGCGGACAGTATCCGTTAGCGGAGGTTGCGAACA 5460
Db 5401 GCCACGCTTCCGAAAGGAGAAAGGCGGACAGTATCCGTTAGCGGAGGTTGCGAACA 5460
QY 5461 GAGAGCGCACAGGAGGCTTCCAGGGGGAAACCGCTGTATCTTTATAGTCTCTGCGGG 5520
Db 5461 GAGAGCGCACAGGAGGCTTCCAGGGGGAAACCGCTGTATCTTTATAGTCTCTGCGGG 5520
QY 5521 TTTGCGCACCTCTGACTGAGCGTGCATTTTGTGATGCTGCTGAGGGGGCGGAGCCTA 5580
Db 5521 TTTGCGCACCTCTGACTGAGCGTGCATTTTGTGATGCTGCTGAGGGGGCGGAGCCTA 5580
QY 5581 TGGAAAAAGCGCACAGCGGCTTTTACGTTTCTGCTGCTTCTGCTGCTTTTGTCT 5640
Db 5581 TGGAAAAAGCGCACAGCGGCTTTTACGTTTCTGCTGCTTCTGCTGCTTTTGTCT 5640

QY 5641 CACATGTTCTTCTCGGTTATCCCTGATTCTGTGATAACCGTATTACCGCCTTTGAG 5700
Db 5641 CACATGTTCTTCTCGGTTATCCCTGATTCTGTGATAACCGTATTACCGCCTTTGAG 5700
QY 5701 TGAGCTGATACCGCTCCCGCAGCCGAAACGACCGAGCGCAGTCAAGTGAGAGGAA 5760
Db 5701 TGAGCTGATACCGCTCCCGCAGCCGAAACGACCGAGCGCAGTCAAGTGAGAGGAA 5760
QY 5761 GCGGAAGAGCGCCCAATACGCAACCGCTCTCCCGCGGCTTGGCCGATTCAATATGC 5820
Db 5761 GCGGAAGAGCGCCCAATACGCAACCGCTCTCCCGCGGCTTGGCCGATTCAATATGC 5820
QY 5821 AG 5822
Db 5821 AG 5822

RESULT 2
US-09-991-209-32
; Sequence 32, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pGt6 vector
US-09-991-209-32

Query Match 47.5%; Score 2768; DB 10; Length 4773;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;
2835 AAGCAGATCGTTCAACATTTGGCAATAAAGTTTCTTAAGATGAATCCTGTTCCGGTC 2894
778 AAGCAGATCGTTCAACATTTGGCAATAAAGTTTCTTAAGATGAATCCTGTTCCGGTC 837
2895 TTGCGATGATTATCATATAATTTCTGTTGAAATTAACGTTAAGCATTAATAATTAACATGT 2954
838 TTGCGATGATTATCATATAATTTCTGTTGAAATTAACGTTAAGCATTAATAATTAACATGT 897
2955 AATGATGACGTTTATGATGAGTGGTTTTATGATGAGTCCCGCAATTAATATATAT 3014
898 AATGATGACGTTTATGATGAGTGGTTTTATGATGAGTCCCGCAATTAATATATAT 957
3015 AATACCGATAGAAAACAAATATAGCGCAAACTAGGATAAATATATCGCGCGGTGT 3074
958 AATACCGATAGAAAACAAATATAGCGCAAACTAGGATAAATATATCGCGCGGTGT 1017
3075 CATCTATGTTACTAGATCGACCTGAGGCAATGGATCCGCGCGGCAATGCGACGTGGGC 3134
1018 CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGGAGC-----T 1064
3135 CCAATTCGCCCTATAGTACTGCTATTAC---AATTCACCTGGCGTCTGTTTACACGTC 3191
1065 CCAATTCGCCCTATAGTACTGCTATTACCGCGCTCACTGGCGCTGTTTACACGTC 1124
3192 GTCACTGGGAAACCCCTGGGCTTACCCAACTAATCGCCTTGACGACATCCCGCTTGC 3251

Db 1125 GTGACTGGGAAACCCCTGGCGTTTACCAACTTAATCGCTTGCAGCACAATCCCCCTTTGG 1184
QY 3252 CCAGCTGGCGTAATAGCGAGAGAGCCCGCAGATCGCCCTTCCCAACAGTTGGCGAGCC 3311
Db 1185 CCAGCTGGCGTAATAGCGAGAGAGAGCCCGCAGATCGCCCTTCCCAACAGTTGGCGAGCC 1244
QY 3312 TGAATGGCGAAT- GGAACGCGCCCTGTAGCGCGCATTAAGCGCGCGCGGTGTGGTGGTTA 3370
Db 1245 TGAATGGCGAATGGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGCGGTGTGGTGGTTA 1304
QY 3371 CGCGGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCGCGCTTTCGCTTTCCTTC 3430
Db 1305 CGCGGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCGCGCTTTCGCTTTCCTTC 1364
QY 3431 CTTCCCTTTCTCGCACGCTTCGCGGCTTTCGCGCTCAAGCTCAAAATCGGGGGCTCCCTT 3490
Db 1365 CTTCCCTTTCTCGCACGCTTCGCGGCTTTCGCGCTCAAGCTCTAAATCGGGGGCTCCCTT 1424
QY 3491 TAGGGTTCGGATTTAGAGCTTTACGGCACCTCGACCGCAAAAAAATTGATTTGGGTGATG 3550
Db 1425 TAGGGTTCGGATTTAGTGTCTTTACGGCACCTCGACCGCAAAAAAATTGATTTGGGTGATG 1484
QY 3551 GTTCAGCTAGTGGCCATCGCCCTGTAGACGCTTTTCGCCCTTTGACGTTGGAGTCCA 3610
Db 1485 GTTCAGCTAGTGGCCATCGCCCTGTAGACGCTTTTCGCCCTTTGACGTTGGAGTCCA 1544
QY 3611 CGTCTTTTAATAGTGGACTCTTGTCCAAACTGGAACACACTCAACCTATCTCGGTCT 3670
Db 1545 CGTCTTTTAATAGTGGACTCTTGTCCAAACTGGAACACACTCAACCTATCTCGGTCT 1604
QY 3671 ATTCTTTGATTTAAGGATTTTCCGATTTTCGCCCTATTGGTTAAAAAATGACTGA 3730
Db 1605 ATTCTTTGATTTAAGGATTTTTCGCCCTATTGGTTAAAAAATGACTGA 1664
QY 3731 TTTTAAACAATAATTAAACGGAATTTTAAACAATAATAACGTTTAAACCTTTCGCTGATG 3790
Db 1665 TTTTAAACAATAATTAAACGGAATTTTAAACAATAATAACGTTTAAACCTTTCGCTGATG 1715
QY 3791 CGGTATTTTCTCTTACGCATCTGTGCGTATTTCACACGGCATACAGTGGCACTTTTC 3850
Db 1716 -----AGGTGGCACTTTTC 1729
QY 3851 GGGGAAATGTGCGGGAACCCCTATTGTGTTATTTTCTAAATAACATTCAAATATGTATC 3910
Db 1730 GGGGAAATGTGCGGGAACCCCTATTGTGTTATTTCTAAATAACATTCAAATATGTATC 1789
QY 3911 CGCTCATGAGCAATAACCTGTAAATGCTTCAATAATATTGAAAGGAGAGATGA 3970
Db 1790 CGCTCATGAGCAATAACCTGTAAATGCTTCAATAATATTGAAAGGAGAGATGA 1849
QY 3971 GTATTCAACATTTCCGTGCGCCCTATTTCCTTTTTCGCGCAATTTGCGCTTCCTGTTT 4030
Db 1850 GTATTCAACATTTCCGTGCGCCCTATTTCCTTTTTCGCGCAATTTGCGCTTCCTGTTT 1909
QY 4031 TTGCTCACCCGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGACACGAG 4090
Db 1910 TTGCTCACCCGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGACACGAG 1969
QY 4091 TGGGTTACATCGAATCTCAACAGCGGTAGATCCTTGAGAGTTTTCGCCCGGAAG 4150
Db 1970 TGGGTTACATCGAATCTCAACAGCGGTAGATCCTTGAGAGTTTTCGCCCGGAAG 2029
QY 4151 AACGTTTTTCCATGATGAGCACTTTTAAAGTTTCTGCTATGTGGCGCGGTATTATCCCGTA 4210
Db 2030 AACGTTTTTCCATGATGAGCACTTTTAAAGTTTCTGCTATGTGGCGCGGTATTATCCCGTA 2089
QY 4211 TTGACGCGCGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAACTGACTTGGTTG 4270
Db 2090 TTGACGCGCGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAACTGACTTGGTTG 2149
QY 4271 AGTACTCACAGTACAGAAAGCATCTTAACGATGGCATGACAGTAAGAGAAATTATGCA 4330
Db 2150 AGTACTCACAGTACAGAAAGCATCTTAACGATGGCATGACAGTAAGAGAAATTATGCA 2209

QY 4331 GTGCTGCCATAAACCATGAGTGATAACAACACTGGGCAACTTACTTCTGCAACGATCGGAG 4390
Db 2210 GTGCTGCCATAAACCATGAGTGATAACAACACTGGGCAACTTACTTCTGCAACGATCGGAG 2269
QY 4391 GACGAGGAGCTTAACCGCTTTTGTGCAACAATGGGGGATCATGTAACTTCGCTTCGATC 4450
Db 2270 GACGAGGAGCTTAACCGCTTTTGTGCAACAATGGGGGATCATGTAACTTCGCTTCGATC 2329
QY 4451 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAACGATGCGTG 4510
Db 2330 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAACGATGCGTG 2389
QY 4511 TAGCAATGGCAACAAACGTTGCGCAAACTATTAACTGCGCAAACTATTAACTGAGTTTCCC 4570
Db 2390 TAGCAATGGCAACAAACGTTGCGCAAACTATTAACTGCGCAAACTATTAACTGAGTTTCCC 2449
QY 4571 GGCACCAATTAATAGACTGGAGCGGATGAAGTTGAGGACCACTTCTCGCTCGG 4630
Db 2450 GGCACCAATTAATAGACTGGAGCGGATGAAGTTGAGGACCACTTCTCGCTCGG 2509
QY 4631 CCCTTCCGCTGGCTGTTTATTGCTGATAAATCTGAGCCGCTGAGCGTGGCTCGCG 4690
Db 2510 CCCTTCCGCTGGCTGTTTATTGCTGATAAATCTGAGCCGCTGAGCGTGGCTCGCG 2569
QY 4691 GTATCATTTGAGCAGCTGGGCGCAGATGTTAAGCCCTCCGCTATCTGAGTTATCTACACGA 4750
Db 2570 GTATCATTTGAGCAGCTGGGCGCAGATGTTAAGCCCTCCGCTATCTGAGTTATCTACACGA 2629
QY 4751 CGGGGAGTCAGCACTATGGATGAAGCAATAGACAGATCGCTGAGATGAGTGCCTCAC 4810
Db 2630 CGGGGAGTCAGCACTATGGATGAAGCAATAGACAGATCGCTGAGATGAGTGCCTCAC 2689
QY 4811 TGATTAAGCATTTGTAACCTGTCAGACCAAGTTTACTCATATATATCTTTAGATTGATTA 4870
Db 2690 TGATTAAGCATTTGTAACCTGTCAGACCAAGTTTACTCATATATATCTTTAGATTGATTA 2749
QY 4871 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAATCTCATGACCA 4930
Db 2750 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAATCTCATGACCA 2809
QY 4931 AAATCCCTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCTGAGAAAAGATCAAAG 4990
Db 2810 AAATCCCTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCTGAGAAAAGATCAAAG 2869
QY 4991 GATCTTCTTGAGATCCTTTTTCGCGCAATCTGCTGCTTGCAGCAACCAACCAAC 5050
Db 2870 GATCTTCTTGAGATCCTTTTTCGCGCAATCTGCTGCTTGCAGCAACCAACCAAC 2929
QY 5051 CGCTACAGCGGTGTTTGTGCGGATCAAGAGCTACCAACTCTTTTTCGAAAGTAA 5110
Db 2930 CGCTACAGCGGTGTTTGTGCGGATCAAGAGCTACCAACTCTTTTTCGAAAGTAA 2989
QY 5111 CTGGCTTCAGCAGAGCGGATGACCAATATCTGCTTCTAGTGTAGCGGTAGTTCGCC 5170
Db 2990 CTGGCTTCAGCAGAGCGGATGACCAATATCTGCTTCTAGTGTAGCGGTAGTTCGCC 3049
QY 5171 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTACAG 5230
Db 3050 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTACAG 3109
QY 5231 TGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGTTTGGATCTCAAGACGATAGTTAC 5290
Db 3110 TGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGTTTGGATCTCAAGACGATAGTTAC 3169
QY 5291 CGGATAAGGCGCAGCGGTGGAACGGGGGTTTCGTGCACACAGCCCGCTTGGAGC 5350
Db 3170 CGGATAAGGCGCAGCGGTGGAACGGGGGTTTCGTGCACACAGCCCGCTTGGAGC 3229
QY 5351 GAACGACCTACACCGAACTGAGTACCTACAGCGTGTAGCTATGAGAAAGCGCAGCTTC 5410
Db 3230 GAACGACCTACACCGAACTGAGTACCTACAGCGTGTAGCTATGAGAAAGCGCAGCTTC 3289

Db	1824	AAGCAGATCGTTCACAACTTGGCAATAAAGTTTCTTAAGATTGAATCCCTGTGCGCGTC	1883
Qy	2895	TTGGGATGATTATCAATTAATTTCTGTGTAATTAACGTTAAGCATGTAATTAATTAACATGT	2954
Db	1884	TTGGGATGATTATCAATTAATTTCTGTGTAATTAACGTTAAGCATGTAATTAATTAACATGT	1943
Qy	2955	AATGCATGACGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTTATACATTT	3014
Db	1944	AATGCATGACGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTTATACATTT	2003
Qy	3015	AATACGGATAGAAAAAATAATATAGCGCGCAAACTAGAGTAATAATATCGCGCGGTGT	3074
Db	2004	AATACGGATAGAAAAAATAATATAGCGCGCAAACTAGAGTAATAATATCGCGCGGTGT	2063
Qy	3075	CATCTATGTTACTAGATCGACTCGAGGATGGGATCGCGCGCGCATGCGACGTCGGGC	3134
Db	2064	CATCTATGTTACTAGATCGATGAGCTTCTAGAGCGCGCGGTGGAGC-----T	2110
Qy	3135	CCAATTCGCCCTATAGTGAGTGGTATTAC---AATTCACCTGGCGGTGGTTTACAAGTC	3191
Db	2111	CCAATTCGCCCTATAGTGAGTGGTATTACGGCGGTCACTGGCGGTGGTTTACAAGTC	2170
Qy	3192	GTGATCGGAAAAACCTCGCGTTTACCCAACTTAATCGCTTGGAGCAGATCCCGCTTTCG	3251
Db	2171	GTGATCGGAAAAACCTCGCGTTTACCCAACTTAATCGCTTGGAGCAGATCCCGCTTTCG	2230
Qy	3252	CCAGCTGGCGTAATAGCAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCGAGCC	3311
Db	2231	CCAGCTGGCGTAATAGCAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCGAGCC	2290
Qy	3312	TGAATGGCGAAT-GGACGCGCCCTGTAGCGCGCATTTAAGCGCGCGGTGTGGTGTGA	3370
Db	2291	TGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTTAAGCGCGCGGTGTGGTGTGA	2350
Qy	3371	CGCGCAGCGTGAACGCTACACTTGGCAGCGCCCTAGCGCCCGCTCTTTCGTTTCTTCC	3430
Db	2351	CGCGCAGCGTGAACGCTACACTTGGCAGCGCCCTAGCGCCCGCTCTTTCGTTTCTTCC	2410
Qy	3431	CTTCTCTTCTCGCCACGTTTCCCGCTTTCGCGTCAAGCTCTAATCGGGGCTCCCTT	3490
Db	2411	CTTCTCTTCTCGCCACGTTTCCCGCTTTCGCGTCAAGCTCTAATCGGGGCTCCCTT	2470
Qy	3491	TAGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACTTGATTTGGGTGATG	3550
Db	2471	TAGGTTCCGATTTAGTGCTTTACGGCACCTCGACCGCAAAAACTTGATTTGGGTGATG	2530
Qy	3551	GTTCACGATGGGCGCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCA	3610
Db	2531	GTTCACGATGGGCGCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCA	2590
Qy	3611	CGTTCTTTAATAGTCGACTCTTGTTCGAACTGGAAACACACTCAACCTATCTCGGTCT	3670
Db	2591	CGTTCTTTAATAGTCGACTCTTGTTCGAACTGGAAACACACTCAACCTATCTCGGTCT	2650
Qy	3671	ATTCCTTTTGAITTAAGGGAATTTTCGCGATTTTCGCCCTTATTTGGTTAAAAAATAGCTGA	3730
Db	2651	ATTCCTTTTGAITTAAGGGAATTTTCGCGATTTTCGCCCTTATTTGGTTAAAAAATAGCTGA	2710
Qy	3731	TTTAAACAAATATTTAAACGGGAATTTTAAACAAATATTAACGTTTAAACGTTTAAACGTTT	3790
Db	2711	TTTAAACAAATATTTAAACGGGAATTTTAAACAAATATTAACGTTTAAACGTTTAAACGTTT	2761
Qy	3791	CGGTATTTCTCTTACGCATCTGTGCGGTATTTACACCGCATACAGGTGGCACTTTTC	3850
Db	2762	-----AGGTGGCACTTTTC	2775
Qy	3851	GGGGAATGTGGCGGAACCCCTATTTGTTTATTTTCTTAAATPAATTAATTAATGATATC	3910
Db	2776	GGGGAATGTGGCGGAACCCCTATTTGTTTATTTTCTTAAATPAATTAATTAATGATATC	2835
Qy	3911	CGCTCATGAGCAATTAACCTGATTAATGCTTCAATATTAATTAATTAATTAATTAATTAATTAAT	3970
Db	2836	CGCTCATGAGCAATTAACCTGATTAATGCTTCAATATTAATTAATTAATTAATTAATTAATTAAT	2895
Qy	3971	GTATTTCAACATTTCCGTGTCCGCTTATTCCTTTTGTGGGGAATTTTTCCTTCTCTGTTT	4030
Db	2896	GTATTTCAACATTTCCGTGTCCGCTTATTCCTTTTGTGGGGAATTTTTCCTTCTCTGTTT	2955
Qy	4031	TTGCTTACCCAGAAACGCTGGTGAAGTAAGATGCTGAAGATCACTGGGTGCACGAG	4090
Db	2956	TTGCTTACCCAGAAACGCTGGTGAAGTAAGATGCTGAAGATCACTGGGTGCACGAG	3015
Qy	4091	TGGTTTACATCGAACTCGATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCCGAG	4150
Db	3016	TGGTTTACATCGAACTCGATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCCGAG	3075
Qy	4151	AACGTTTTCATGATGAGCACTTTTAAAGTTTCTGCTATGTTGGCGCGGTATTTATCCCGTA	4210
Db	3076	AACGTTTTCATGATGAGCACTTTTAAAGTTTCTGCTATGTTGGCGCGGTATTTATCCCGTA	3135
Qy	4211	TTGACGCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTTCTCAGATGACTTGGTTG	4270
Db	3136	TTGACGCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTTCTCAGATGACTTGGTTG	3195
Qy	4271	AGTACTCACAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATATCA	4330
Db	3196	AGTACTCACAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATATCA	3255
Qy	4331	GTGCTGCCATTAACCATGAGTGATTAACACTGCGGCAACTTCTTCTGACAGATCGGAG	4390
Db	3256	GTGCTGCCATTAACCATGAGTGATTAACACTGCGGCAACTTCTTCTGACAGATCGGAG	3315
Qy	4391	GACCGAAGGAGTAAACGCTTTTGGCACAACATGGGGGATCATGTAACTCGCCCTGATC	4450
Db	3316	GACCGAAGGAGTAAACGCTTTTGGCACAACATGGGGGATCATGTAACTCGCCCTGATC	3375
Qy	4451	GTTCGGAACCGGAGCTGAATGAAGCCATACCAACAGCAGCGGTGACACCGATGCTG	4510
Db	3376	GTTCGGAACCGGAGCTGAATGAAGCCATACCAACAGCAGCGGTGACACCGATGCTG	3435
Qy	4511	TAGCAATGGCAACAACTGCGGCAAACTAATTAACCTGGCGAACTACTTACTCTAGCTTCCC	4570
Db	3436	TAGCAATGGCAACAACTGCGGCAAACTAATTAACCTGGCGAACTACTTACTCTAGCTTCCC	3495
Qy	4571	GGCAACAAATTAAGTACGTTGAGTGAAGCGGATGAGCGGATGAGCGGATGAGCGGATGAGCGG	4630
Db	3496	GGCAACAAATTAAGTACGTTGAGTGAAGCGGATGAGCGGATGAGCGGATGAGCGGATGAGCGG	3555
Qy	4631	CCCTTCCGCTGGCTGGTTTATTTGCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCGCG	4690
Db	3556	CCCTTCCGCTGGCTGGTTTATTTGCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCGCG	3615
Qy	4691	GTATCATTTGACGACTGGGCGCAGATGTAAGCCCTCCGCTATCGTAGTATCTACACGA	4750
Db	3616	GTATCATTTGACGACTGGGCGCAGATGTAAGCCCTCCGCTATCGTAGTATCTACACGA	3675
Qy	4751	CGGGAGTCAAGCACTATGATGAACGAAATAGACAGATCGCTCAGATAGTGGCTCAC	4810
Db	3676	CGGGAGTCAAGCACTATGATGAACGAAATAGACAGATCGCTCAGATAGTGGCTCAC	3735
Qy	4811	TGATTAAGCAATTTGATTAAGCAATTTGATTAAGCAATTTGATTAAGCAATTTGATTAAGCAATTT	4870
Db	3736	TGATTAAGCAATTTGATTAAGCAATTTGATTAAGCAATTTGATTAAGCAATTTGATTAAGCAATTT	3795
Qy	4871	AACCTTCAATTTTAAATTAAGGATCTAGTGAAGATCGTTTGTGATTAATCTCATGACCA	4930
Db	3796	AACCTTCAATTTTAAATTAAGGATCTAGTGAAGATCGTTTGTGATTAATCTCATGACCA	3855
Qy	4931	AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAAGATCAAAAG	4990
Db	3856	AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAAGATCAAAAG	3915
Qy	4991	GATCTTCTTGAGATCCTTTTTCGCGGTAAATCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT	5050
Db	3916	GATCTTCTTGAGATCCTTTTTCGCGGTAAATCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCT	3975

```
QY 5051 CGCTACAGCGGTGGTTGTTGGCGGATCAAGAGCTACCAACTCTTTTCCGAAGTAA 5110
Db CGCTACAGCGGTGGTTGTTGGCGGATCAAGAGCTACCAACTCTTTTCCGAAGTAA 4035
QY 5111 CTGGCTTCACAGAGCGCAGATACCAATACTGCTCTTCTAGTGTAGCGTAGTTAGGCC 5170
Db CTGGCTTCACAGAGCGCAGATACCAATACTGCTCTTCTAGTGTAGCGTAGTTAGGCC 4095
QY 5171 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTACCAG 5230
Db ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTACCAG 4155
QY 5231 TGCGTCTGCAGTGGCGATPAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTAC 5290
Db TGCGTCTGCAGTGGCGATPAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTAC 4215
QY 5291 CGGATAAGCGGACGGTGGGCTGAACCGGGGGTTCGTGCAACAGCCAGCTTGGAGC 5350
Db CGGATAAGCGGACGGTGGGCTGAACCGGGGGTTCGTGCAACAGCCAGCTTGGAGC 4275
QY 5351 GAAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTTCGGAAACAGAGAGCGCA 5410
Db GAAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTTCGGAAACAGAGAGCGCA 4335
QY 5411 CCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGCGGTTCGGAAACAGAGAGCGCA 5470
Db CCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGCGGTTCGGAAACAGAGAGCGCA 4395
QY 5471 CGAGGAGGCTTCAGGGGAAACCGCTGATCTTTATAGTCTGTCGGGTTCGCCACC 5530
Db CGAGGAGGCTTCAGGGGAAACCGCTGATCTTTATAGTCTGTCGGGTTCGCCACC 4455
QY 5531 TCTGACTTGAGCGTGGATTTTGTGATGCTCGTCAGGGGGGCGAGCCATAGAAAAACG 5590
Db TCTGACTTGAGCGTGGATTTTGTGATGCTCGTCAGGGGGGCGAGCCATAGAAAAACG 4515
QY 5591 CCAGCAACCGCGCTTTTACGGTCTTCTGGCCCTTTGCTGGCCCTTTGCTCAGATGTTCT 5650
Db CCAGCAACCGCGCTTTTACGGTCTTCTGGCCCTTTGCTGGCCCTTTGCTCAGATGTTCT 4575
QY 5651 TTCTCGGCTATCCCTGATCTCTGTGGATAACCGTATTACCGCTTTGAGTGAAGTATA 5710
Db TTCTCGGCTATCCCTGATCTCTGTGGATAACCGTATTACCGCTTTGAGTGAAGTATA 4635
QY 5711 CGCTCGCGCAGCGCAACCGAGCGCAGCGAGTCACTGAGCGAGGAGCGGAGAGC 5770
Db CGCTCGCGCAGCGCAACCGAGCGCAGCGAGTCACTGAGCGAGGAGCGGAGAGC 4695
QY 5771 GCCCAATACGCAACCGCTCTCCCGCGGCTTGGCCGATTCATTAATGCGAG 5822
Db GCCCAATACGCAACCGCTCTCCCGCGGCTTGGCCGATTCATTAATGCGAG 4747
```

RESULT 5

```
US-09-991-209-35
; Sequence 35, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Philip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC48-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 4974
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJQ4 vector
US-09-991-209-35
```

Query Match 47.5%; Score 2768; DB 10; Length 4974;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

```
QY 2835 AAGCAGATCGTTCCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTC 2894
Db 1833 AAGCAGATCGTTCCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTC 1892
QY 2895 TTGCGATGATTATCATATAATTTCTGTGAAATACGTTAAGCATGTAAATAATTAACATGT 2954
Db 1893 TTGCGATGATTATCATATAATTTCTGTGAAATACGTTAAGCATGTAAATAATTAACATGT 1952
QY 2955 AATGCATGACGTTATTTATGAGATGGGTTTTTAAGATTAGAGTCCCGCAATTATACATTT 3014
Db 1953 AATGCATGACGTTATTTATGAGATGGGTTTTTAAGATTAGAGTCCCGCAATTATACATTT 2012
QY 3015 AATACCGCATAGAAAAAATAATATAGCGCGCAAACTAGGATAAATTTATCGCGCGCGTGT 3074
Db 2013 AATACCGCATAGAAAAAATAATATAGCGCGCAAACTAGGATAAATTTATCGCGCGCGTGT 2072
QY 3075 CATCTATGTTACTAGATCGACCTCGAGGATCGGATCCCGCGCGCATGCGACGTCGGGC 3134
Db 2073 CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGAGC-----T 2119
QY 3135 CCAATTCGCCCTATAGTGTAGTCTGTAATTAC---AATCTACGTGGCGGTCGTTTACAAAGTC 3191
Db 2120 CCAATTCGCCCTATAGTGTAGTCTGTAATTACGCGCGCTCACTGGCGGTCGTTTACAAAGTC 2179
QY 3192 GTGACTGGGAAACCTCGCGTTACCAACTTTAATGCCCTTGAGCAGCATCCCCCTTTCG 3251
Db 2180 GTGACTGGGAAACCTCGCGTTACCAACTTTAATGCCCTTGAGCAGCATCCCCCTTTCG 2239
QY 3252 CCAGCTGGCGTAATAGCAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCC 3311
Db 2240 CCAGCTGGCGTAATAGCAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCC 2299
QY 3312 TGAATGGCGAAT- GAGCGGCGCTGTAGCGCGCATTAAGCGCGGCGGTGTGGTTA 3370
Db 2300 TGAATGGCGAATGGGACGCGCCTGTAGCGCGCATTAAGCGCGGCGGTGTGGTTA 2359
QY 3371 CGCGCAGGTGACCGCTACACTTGCAGCGCCCTAGCGCGCCTCTTCGCTTCTTCCTCC 3430
Db 2360 CGCGCAGGTGACCGCTACACTTGCAGCGCCCTAGCGCGCCTCTTCGCTTCTTCCTCC 2419
QY 3431 CTTCCCTTTCGCCACAGTTTCGCCGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTT 3490
Db 2420 CTTCCCTTTCGCCACAGTTTCGCCGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTT 2479
QY 3491 TAGGTTCCGATTTAGAGCTTTACGGACCTCGACCGCAAAAAAATCTGATTGGGTGATG 3550
Db 2480 TAGGTTCCGATTTAGAGCTTTACGGACCTCGACCGCAAAAAAATCTGATTGGGTGATG 2539
QY 3551 GTTCACGTAGTGGGCCATCGCCCTGATAGAGCGTTTTCGCCCTTTCGACGTTGAGTCCA 3610
Db 2540 GTTCACGTAGTGGGCCATCGCCCTGATAGAGCGTTTTCGCCCTTTCGACGTTGAGTCCA 2599
QY 3611 CGTCTTTTAATAGTGAAGTCTTGTTCGCAAACTGGAACAACTCAACCTCTCTCGGTCT 3670
Db 2600 CGTCTTTTAATAGTGAAGTCTTGTTCGCAAACTGGAACAACTCAACCTCTCTCGGTCT 2659
QY 3671 ATTCCTTTGATTATAAGGATTTTCCGATTTCCGCTATTCGTTGTTAAAAAATGAGTGA 3730
Db 2660 ATTCCTTTGATTATAAGGATTTTCCGATTTCCGCTATTCGTTGTTAAAAAATGAGTGA 2719
QY 3731 TTTAACAAATATTTAACGCGAATTTTAAACAAATATTAAGCTTTTACATTTTCGCTGATG 3790
Db 2720 TTTAACAAATATTTAACGCGAATTTTAAACAAATATTAAGCTTTTACATTT-----T 2770
```

QY 3791 CGGTAATTTCTCCTTACGCAATCTGTGGGTATTTTACACCGCATACAGGTGGCACTTTTC 3850
Db 2771 -----AGGTGGCACTTTTC 2784
QY 3851 GGGGAATGTGGCGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGTATC 3910
Db 2785 GGGGAATGTGGCGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGTATC 2844
QY 3911 CGCTCATGAGACAATAACCCCTGATPAATGCTTCAATATATTTGAAAAGGAAGATGA 3970
Db 2845 CGCTCATGAGACAATAACCCCTGATPAATGCTTCAATATATTTGAAAAGGAAGATGA 2904
QY 3971 GTATTCAACATTTCCGTTGCGCCCTATTCCCTTTTGGCGCAATTTTCCCTCTCTTT 4030
Db 2905 GTATTCAACATTTCCGTTGCGCCCTATTCCCTTTTGGCGCAATTTTCCCTCTCTTT 2964
QY 4031 TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 4090
Db 2965 TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 3024
QY 4091 TGGGTTATCATCGAATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGGAG 4150
Db 3025 TGGGTTATCATCGAATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGGAG 3084
QY 4151 AACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTA 4210
Db 3085 AACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTA 3144
QY 4211 TTGACCGCGGCAAGAGCAACTCGGTGCGCCGATACACTATTTCTCAGAAATGACTGGTGTG 4270
Db 3145 TTGACCGCGGCAAGAGCAACTCGGTGCGCCGATACACTATTTCTCAGAAATGACTGGTGTG 3204
QY 4271 AGTACTACCAAGTCAAGAAAGCACTTTACGATGGCATGACAGTAAGAAATTTATGCA 4330
Db 3205 AGTACTACCAAGTCAAGAAAGCACTTTACGATGGCATGACAGTAAGAAATTTATGCA 3264
QY 4331 GTGCTGCCATACCAATGATGATACACTGCGGCCAACTTACTTCTGCAACGATCGGAG 4390
Db 3265 GTGCTGCCATACCAATGATGATACACTGCGGCCAACTTACTTCTGCAACGATCGGAG 3324
QY 4391 GACCGAAGAGGTAACCGCTTTTTCACAAACATGGGGATCATGTAACCTGCCCTTGATC 4450
Db 3325 GACCGAAGAGGTAACCGCTTTTTCACAAACATGGGGATCATGTAACCTGCCCTTGATC 3384
QY 4451 GTTGGAAACCGGAGTGAATGAAGCCATACCAACGACGAGCGTGACACCCAGATGCCCTG 4510
Db 3385 GTTGGAAACCGGAGTGAATGAAGCCATACCAACGACGAGCGTGACACCCAGATGCCCTG 3444
QY 4511 TAGCAATGCAACACGTTGCGCAACATTAACCTGCGGAACTTACTTACTTAGCTTCCC 4570
Db 3445 TAGCAATGCAACACGTTGCGCAACATTAACCTGCGGAACTTACTTACTTAGCTTCCC 3504
QY 4571 GGCACAAATTAATAGACTGGATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGG 4630
Db 3505 GGCACAAATTAATAGACTGGATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGG 3564
QY 4631 CCCTTCGCGCTGGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCG 4690
Db 3565 CCCTTCGCGCTGGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCG 3624
QY 4691 GTATCATTTGACACCTGGGCGCAGATGTTAAGCCCTCCGCTATGCTAGTTATTCACGCA 4750
Db 3625 GTATCATTTGACACCTGGGCGCAGATGTTAAGCCCTCCGCTATGCTAGTTATTCACGCA 3684
QY 4751 CGGGAGTCAGGCAACTATGGATGAACGAATAGACAGATCGCTGAGATAGTGGCTTAC 4810
Db 3685 CGGGAGTCAGGCAACTATGGATGAACGAATAGACAGATCGCTGAGATAGTGGCTTAC 3744
QY 4811 TGATTAAGCATTTGGTAACTGTGACACCAAGTTTACTCATATATACATTTAGATTGATTA 4870
Db 3745 TGATTAAGCATTTGGTAACTGTGACACCAAGTTTACTCATATATACATTTAGATTGATTA 3804

QY 4871 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAATCTCATGACCA 4930
Db 3805 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAATCTCATGACCA 3864
QY 4931 AANTCCCTTAACTGAGTTTTTCCACATGAGCGTCAGACCCCGTAGAAAAAGATCAAG 4990
Db 3865 AANTCCCTTAACTGAGTTTTTCCACATGAGCGTCAGACCCCGTAGAAAAAGATCAAG 3924
QY 4991 GATCTTCTTGAGATCCTTTTCTGCGCGTAATCTGCTGTCGCAACAAAAAACCCAC 5050
Db 3925 GATCTTCTTGAGATCCTTTTCTGCGCGTAATCTGCTGTCGCAACAAAAAACCCAC 3984
QY 5051 CGCTACAGCGGTGTTTTTGGCCGATCAAGAGCTACCAACTCTTTTCCGAAAGGTAA 5110
Db 3985 CGCTACAGCGGTGTTTTTGGCCGATCAAGAGCTACCAACTCTTTTCCGAAAGGTAA 4044
QY 5111 CTGCTTCAGCAGCGCAGATACCAATACTGCTCTTCTAGTGTAGCCGTTAGTGGCC 5170
Db 4045 CTGCTTCAGCAGCGCAGATACCAATACTGCTCTTCTAGTGTAGCCGTTAGTGGCC 4104
QY 5171 ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTCTATCTCTGTATTAC 5230
Db 4105 ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTCTATCTCTGTATTAC 4164
QY 5231 TGGCTGCTGCCAGTGGCGATTAAGTCTTACCGGTTTGGACTCAAGACGATAGTTAC 5290
Db 4165 TGGCTGCTGCCAGTGGCGATTAAGTCTTACCGGTTTGGACTCAAGACGATAGTTAC 4224
QY 5291 CGGATAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTCACACAGCCCGTGGAGC 5350
Db 4225 CGGATAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTCACACAGCCCGTGGAGC 4284
QY 5351 GAAACGACCTACACCGAACTGAGATACCTTACAGGCTGATGAGAAAGCGCCGCTTC 5410
Db 4285 GAAACGACCTACACCGAACTGAGATACCTTACAGGCTGATGAGAAAGCGCCGCTTC 4344
QY 5411 CCGAAGGAGAAAGCGGACAGGATTCGGTAAAGCGGAGCGTCCGAAACAGAGAGCGCA 5470
Db 4345 CCGAAGGAGAAAGCGGACAGGATTCGGTAAAGCGGAGCGTCCGAAACAGAGAGCGCA 4404
QY 5471 CGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTCTCGGGTTTCGCCACC 5530
Db 4405 CGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTCTCGGGTTTCGCCACC 4464
QY 5531 TCTGACTTGAGCGTCGATTTTGTGATCTGTCAGGGGGCGGAGCCCTATCGAAAAACG 5590
Db 4465 TCTGACTTGAGCGTCGATTTTGTGATCTGTCAGGGGGCGGAGCCCTATCGAAAAACG 4524
QY 5591 CCAGCAACCGCGCTTTTACGGTTCTGCGCTTTTGTGCTGCTCATGTTCT 5650
Db 4525 CCAGCAACCGCGCTTTTACGGTTCTGCGCTTTTGTGCTGCTCATGTTCT 4584
QY 5651 TTCTCTGCTTATCCCTGATTTCTGTGGATAACCGTATTATACCGCTTTGAGTGGCTGATA 5710
Db 4585 TTCTCTGCTTATCCCTGATTTCTGTGGATAACCGTATTATACCGCTTTGAGTGGCTGATA 4644
QY 5711 CGGCTCGCGCAGCGCAACAGCCGAGCGGAGTCACTGAGCGGAGGAGCGGAGAGC 5770
Db 4645 CGGCTCGCGCAGCGCAACAGCCGAGCGGAGTCACTGAGCGGAGGAGCGGAGAGC 4704
QY 5771 GCCCAATAGCAACCGCCTCTCCCGCGGTTGGCCGATTTCATTAATGAG 5822
Db 4705 GCCCAATAGCAACCGCCTCTCCCGCGGTTGGCCGATTTCATTAATGAG 4756

RESULT 6
US-09-991-209-40
; Sequence 40, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: London, Timothy
; APPLICANT: Morse, Phillip

QY	4631	CCCTTCGGCTGGCTGTTTATTGCTGATAAATCTGAGCGCGGTGAGCGTGGCTCTCGCG	4690
Db	3588	CCCTTCGGCTGGCTGTTTATTGCTGATAAATCTGAGCGCGGTGAGCGTGGCTCTCGCG	3647
QY	4691	GTATCATTTGAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTTATCTACAG	4750
Db	3648	GTATCATTTGAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTTATCTACAG	3707
QY	4751	CGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCAC	4810
Db	3708	CGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCAC	3767
QY	4811	TGATTAGCATTTGGTAAGTCTGACCAAGTTTACTCATATATATATCTTATGATGATTTAA	4870
Db	3768	TGATTAGCATTTGGTAAGTCTGACCAAGTTTACTCATATATATCTTATGATGATTTAA	3827
QY	4871	AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATGACCA	4930
Db	3828	AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATGACCA	3887
QY	4931	AAATCCCTTAACGTGAGTTTTCGTTCACTGAGCGTCAGACCCCGTAGAAGATCAAG	4990
Db	3888	AAATCCCTTAACGTGAGTTTTCGTTCACTGAGCGTCAGACCCCGTAGAAGATCAAG	3947
QY	4991	GATCTTCTGAGATCCCTTTTCTGCGCGTAATCTGCTGTGCAAAACAAAAAACAC	5050
Db	3948	GATCTTCTGAGATCCCTTTTCTGCGCGTAATCTGCTGTGCAAAACAAAAAACAC	4007
QY	5051	CGTACCAAGCGGTGGTTTGTGCGGATCAAGACTACCACTCTTTTTCGAAGGTAA	5110
Db	4008	CGTACCAAGCGGTGGTTTGTGCGGATCAAGACTACCACTCTTTTTCGAAGGTAA	4067
QY	5111	CTGGCTTCAGACAGCGCAGATACCAATACCTGCTCTCTAGTGAGCGTAGTTAGGCC	5170
Db	4068	CTGGCTTCAGACAGCGCAGATACCAATACCTGCTCTCTAGTGAGCGTAGTTAGGCC	4127
QY	5171	ACCCTTCAAGAACTCTGTAGCACCGCTACATACCTGCTCTGTAATCTCTGTTTACAG	5230
Db	4128	ACCCTTCAAGAACTCTGTAGCACCGCTACATACCTGCTCTGTAATCTCTGTTTACAG	4187
QY	5231	TGGCTGCTGCCAGTGGCGATAGTCTGTCTTACCGGTTTGAACCTCAAGACGATAGTTAC	5290
Db	4188	TGGCTGCTGCCAGTGGCGATAGTCTGTCTTACCGGTTTGAACCTCAAGACGATAGTTAC	4247
QY	5291	CGGATAAGCGCAGCGGTGGCTGAAACGGGGGTTCTGTGCACACAGCCAGCTTGGAGC	5350
Db	4248	CGGATAAGCGCAGCGGTGGCTGAAACGGGGGTTCTGTGCACACAGCCAGCTTGGAGC	4307
QY	5351	GAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCAGCTTC	5410
Db	4308	GAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCAGCTTC	4367
QY	5411	CCGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGAGGGTGGAAACAGGAGACGCA	5470
Db	4368	CCGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGAGGGTGGAAACAGGAGACGCA	4427
QY	5471	CGAGGAGCTTCAGGGGAAACCGCTGCTATCTTATAGTCTGCTGCGTTCGCGCAC	5530
Db	4428	CGAGGAGCTTCAGGGGAAACCGCTGCTATCTTATAGTCTGCTGCGTTCGCGCAC	4487
QY	5531	TCTGACTTCAGCGTCCGATTTTGTGATGCTGCTGAGGGGGCGGAGCCTATGAAAAACG	5590
Db	4488	TCTGACTTCAGCGTCCGATTTTGTGATGCTGCTGAGGGGGCGGAGCCTATGAAAAACG	4547
QY	5591	CCAGCAACCGCGCTTTTACGTTCTGCGCTTTTGTGCTGGCTTTTGTCTCATGCTCT	5650
Db	4548	CCAGCAACCGCGCTTTTACGTTCTGCGCTTTTGTGCTGGCTTTTGTCTCATGCTCT	4607
QY	5651	TTCTGCTGTTATCCCTGATTTCTGTGATAACCGTATTACCGCTTTTGTGAGTGTGATA	5710
Db	4608	TTCTGCTGTTATCCCTGATTTCTGTGATAACCGTATTACCGCTTTTGTGAGTGTGATA	4667
QY	5711	CCGCTCGCGCAGCGCAACCGAGCGAGCGAGTCAAGTGAAGCGGAAAGCGGAGAGC	5770

Db

4668

CCCTTCGGCGCAGCCGAAACGACGAGCGGCGAGTCAAGTGAAGGAGGAGCGAAGCAGC

4727

QY

5771

GCCCAATAGCAAAACCGCCTCTCCCGCGCGTTGGCGGATTCATTAATGAGCAG

5822

Db

4728

GCCCAATAGCAAAACCGCCTCTCCCGCGCGTTGGCGGATTCATTAATGAGCAG

4779

RESULT 7

US-09-991-209-33

Sequence 33, Application US/09991209

Publication No. US20030024009A1

GENERAL INFORMATION:

APPLICANT: Dunn-Coleman, Nigel

APPLICANT: Langdon, Timothy

APPLICANT: Morse, Phillip

TITLE OF INVENTION: Manipulation of the Phenolic Acid

TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted

TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes

FILE REFERENCE: GC648-2

CURRENT APPLICATION NUMBER: US/09/991,209

PRIOR FILING DATE: 2002-07-02

PRIOR APPLICATION NUMBER: US 60/249,608

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 33

LENGTH: 5034

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: pJQ5 vector

US-09-991-209-33

Query Match

Best Local Similarity 47.5%; Score 2768; DB 10; Length 5034;

Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY

2835

AAGCAGATCGTTCAAAACATTTGGCAATTAAGTTTCTTAAGATTGAATCTGTTCGGGTC

2894

Db

1889

AAGCAGATCGTTCAAAACATTTGGCAATTAAGTTTCTTAAGATTGAATCTGTTCGGGTC

1948

QY

2895

TTGCGATGATTATCATATAATTTCTGTTGAATTAGTTAAGCATGTAATAATAACATGT

2954

Db

1949

TTGCGATGATTATCATATAATTTCTGTTGAATTAGTTAAGCATGTAATAATAACATGT

2008

QY

2955

AATGATGACGTTATTTATGATGGTTTTTATGATGAGTCCCGCAATTTATACATTT

3014

Db

2009

AATGATGACGTTATTTATGATGGTTTTTATGATGAGTCCCGCAATTTATACATTT

2068

QY

3015

AATACGCGATAGAAACAAATATATAGCGCGCAAACTAGGATAAATATCGCGCGGTGT

3074

Db

2069

AATACGCGATAGAAACAAATATATAGCGCGCAAACTAGGATAAATATCGCGCGGTGT

2128

QY

3075

CATCTATGTTACTAGATCGACCTCGAGGCGATGGATCCCGCGCGCATGCGACGTCGGGC

3134

Db

2129

CATCTATGTTACTAGATCGATAGCTTCTAGAGCGGCGGTGAGC-----T

2175

QY

3135

CAATTCGCGCTTATAGTGTGATTAAC---AATTCATGCGCGTTCGTTTACAAGTC

3191

Db

2176

CAATTCGCGCTTATAGTGTGATTAAC---AATTCATGCGCGTTCGTTTACAAGTC

2235

QY

3192

GTGACTGGGAAACCCCTGGGTTTACCACTTAATCGCTTTCAGCACATCCCTTTCG

3251

Db

2236

GTGACTGGGAAACCCCTGGGTTTACCACTTAATCGCTTTCAGCACATCCCTTTCG

2295

QY

3252

CCAGCTGGCGTATAGCGAAGAGCGCGCACCGCATGCCCTTCCCAACAGTTGCGCAGCC

3311

Db

2296

CCAGCTGGCGTATAGCGAAGAGCGCGCACCGCATGCCCTTCCCAACAGTTGCGCAGCC

2355

QY

3312

TGAATGCGCAAT--GGAACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGTGA

3370

Db

2356

TGAATGCGCAATGGGACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGTGA

2415

QY 3371 CGCGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTTCGCTTCTTCC 3430
Db 2416 CGCGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTTCGCTTCTTCC 2475
QY 3431 CTTTCCTTCTCGGCAAGCTTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTT 3490
Db 2476 CTTTCCTTCTCGGCAAGCTTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTT 2535
QY 3491 TAGGTTTCGATTTAGAGCTTTACGGCACTTCAGCGCTTTCGCCCTTTGACGCTTCGAGTCCA 3550
Db 2536 TAGGTTTCGATTTAGGCTTTACGGCACTTCAGCGCTTTCGCCCTTTGACGCTTCGAGTCCA 2595
QY 3551 GTTTCAGTGTGGGCCATCGCCCTGATAGAGCTTTTCGCCCTTTGACGCTTCGAGTCCA 3610
Db 2596 GTTTCAGTGTGGGCCATCGCCCTGATAGAGCTTTTCGCCCTTTGACGCTTCGAGTCCA 2655
QY 3611 CGTTCTTTAATAGTGACTCTTGTTCGAACTGGAACCAACCTTATCTCGGTCT 3670
Db 2656 CGTTCTTTAATAGTGACTCTTGTTCGAACTGGAACCAACCTTATCTCGGTCT 2715
QY 3671 ATTCTTTTGTATTTAAGGATTTTCGCGATTTTCGCGCTTATGGTTTAAAAAATGAGCTGA 3730
Db 2716 ATTCTTTTGTATTTAAGGATTTTCGCGATTTTCGCGCTTATGGTTTAAAAAATGAGCTGA 2775
QY 3731 TTTAACAAATATTTAACGGAATTTTAAACAAATATTTAACGTTTACAAATTTTCGCTGATG 3790
Db 2776 TTTAACAAATATTTAACGGAATTTTAAACAAATATTTAACGTTTACAAATTTTCGCTGATG 2826
QY 3791 CGGTATTTCTCTTACGCACTGTGCGGTATTTTACACCGCATACAGGTGGCACTTTTC 3850
Db 2827 -----AGTGGCACTTTTC 2840
QY 3851 GGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAATATCAATCAATATGATATC 3910
Db 2841 GGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAATATCAATCAATATGATATC 2900
QY 3911 CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATATATTTGAAAGGAAGATGATGA 3970
Db 2901 CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATATATTTGAAAGGAAGATGATGA 2960
QY 3971 GTATTTCAATTTTCGTTGCGGCTTATTCCTTTTTCGCGCATTTTGCCCTTCCTGTTT 4030
Db 2961 GTATTTCAATTTTCGTTGCGGCTTATTCCTTTTTCGCGCATTTTGCCCTTCCTGTTT 3020
QY 4031 TTGCTCACCGAAGACGCTGTGGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG 4090
Db 3021 TTGCTCACCGAAGACGCTGTGGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG 3080
QY 4091 TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGAAG 4150
Db 3081 TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGAAG 3140
QY 4151 AACGTTTTCGAATGATGACCTTTTAAAGTCTGCTATGTGGCGGCTATTTATCCCGTA 4210
Db 3141 AACGTTTTCGAATGATGACCTTTTAAAGTCTGCTATGTGGCGGCTATTTATCCCGTA 3200
QY 4211 TTGACGCGGSCAAGAGCACTCGGTGCGGCTATACATCTCTCAGATGACTTGGTTG 4270
Db 3201 TTGACGCGGSCAAGAGCACTCGGTGCGGCTATACATCTCTCAGATGACTTGGTTG 3260
QY 4271 AGTACTCACCAAGTACAGAAAGCATCTTACGGATGGCATGACATGAGAAATTTATGCA 4330
Db 3261 AGTACTCACCAAGTACAGAAAGCATCTTACGGATGGCATGACATGAGAAATTTATGCA 3320
QY 4331 GTGCTGCCATACCAATGATGATTAACACTGCGGCACTTTACTTCTGACAAAGATGCGAG 4390
Db 3321 GTGCTGCCATACCAATGATGATTAACACTGCGGCACTTTACTTCTGACAAAGATGCGAG 3380
QY 4391 GACCGAAGGACTTAACCGCTTTTTCGACAACTGCGGGAATCATGTAATCGCTTGTATC 4450
Db 3381 GACCGAAGGACTTAACCGCTTTTTCGACAACTGCGGGAATCATGTAATCGCTTGTATC 3440

QY 4451 GTTGGAAACCGAGCTGAATGAAGCCATATACAAACGACGAGCTGACACCAAGTGCCTG 4510
Db 3441 GTTGGAAACCGAGCTGAATGAAGCCATATACAAACGACGAGCTGACACCAAGTGCCTG 3500
QY 4511 TAGCAATGGCAACAAAGTTCGCGCAAACTATTAATCTGCGAACTACTTACTCTAGCTTCCC 4570
Db 3501 TAGCAATGGCAACAAAGTTCGCGCAAACTATTAATCTGCGAACTACTTACTCTAGCTTCCC 3560
QY 4571 GGCAACAAATTAATAGACTGATGAGCGGATAAAGTTGCGAGCACTTCTCGCTCGG 4630
Db 3561 GGCAACAAATTAATAGACTGATGAGCGGATAAAGTTGCGAGCACTTCTCGCTCGG 3620
QY 4631 CCCTTCGCGCTCGCTCGCTTATTTGCTGATTAATCTGAGCCGCTGAGCGGTCTCGCG 4690
Db 3621 CCCTTCGCGCTCGCTCGCTTATTTGCTGATTAATCTGAGCCCTCGCTGATGCTGAGTCTCGCG 3680
QY 4691 GTATCATTTGAGCACTTGGGCGCAGATGTTAAGCCCTCCGCTATCTGATCTACACGA 4750
Db 3681 GTATCATTTGAGCACTTGGGCGCAGATGTTAAGCCCTCGCTGATCTGATCTACACGA 3740
QY 4751 CGGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCAC 4810
Db 3741 CGGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCAC 3800
QY 4811 TGATTAAGCAATTTGGTAACTGTGAGCAAAAGTTTACTCATATATACTTTAGATTGATTAA 4870
Db 3801 TGATTAAGCAATTTGGTAACTGTGAGCAAAAGTTTACTCATATATACTTTAGATTGATTAA 3860
QY 4871 AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTATATCTCATGACCA 4930
Db 3861 AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTATATCTCATGACCA 3920
QY 4931 AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGCTCAGACCCGCTAGAAAAAGATCAAG 4990
Db 3921 AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGCTCAGACCCGCTAGAAAAAGATCAAG 3980
QY 4991 GATCTCTTGAGATCTCTTTTCTGCGGTAATCTGCTGCTTGCATAACAAAAACCAAC 5050
Db 3981 GATCTCTTGAGATCTCTTTTCTGCGGTAATCTGCTGCTTGCATAACAAAAACCAAC 4040
QY 5051 CGCTACCAAGCGGTGTTTGTGCGGATCAAGAGTCAACACTCTTTTCCGAAAGTTAA 5110
Db 4041 CGCTACCAAGCGGTGTTTGTGCGGATCAAGAGTCAACACTCTTTTCCGAAAGTTAA 4100
QY 5111 CTGGCTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCTGCTAATCTCTGTTTACCAAG 5170
Db 4101 CTGGCTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCTGCTAATCTCTGTTTACCAAG 4160
QY 5171 ACCACTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCTGCTAATCTCTGTTTACCAAG 5230
Db 4161 ACCACTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCTGCTAATCTCTGTTTACCAAG 4220
QY 5231 TGGCTGCTGCCAGTGGCGATTAAGTCTGCTTCTACCGGTTGAGCTCAAGAGATAGTTAC 5290
Db 4221 TGGCTGCTGCCAGTGGCGATTAAGTCTGCTTCTACCGGTTGAGCTCAAGAGATAGTTAC 4280
QY 5291 CGGATAAGGCGCAGCGGTGCGGCTGAAACGCGGCTGAAACGCGGCTGAAACGCGGCTGAAAC 5350
Db 4281 CGGATAAGGCGCAGCGGTGCGGCTGAAACGCGGCTGAAACGCGGCTGAAACGCGGCTGAAAC 4340
QY 5351 GAAACGCTTACCGAACTGAGATACCTACAGCGGTGAGCTATGAGAAAGCGCCAGCTTC 5410
Db 4341 GAAACGCTTACCGAACTGAGATACCTACAGCGGTGAGCTATGAGAAAGCGCCAGCTTC 4400
QY 5411 CCGAAGGAGAAAGCGCGACAGGATCCGTTAAGCGGCTGAGCTGAGAAAGCGCCAGCTTC 5470
Db 4401 CCGAAGGAGAAAGCGCGACAGGATCCGTTAAGCGGCTGAGCTGAGAAAGCGCCAGCTTC 4460
QY 5471 CGAGGAGCTTCCAGGGGAAACCGCTTGTATCTTTTATAGTCTCTCGGTTTCGCCAC 5530
Db 4461 CGAGGAGCTTCCAGGGGAAACCGCTTGTATCTTTTATAGTCTCTCGGTTTCGCCAC 4520
QY 5531 TCTGACTTGAGCTCGATTTTGTGATGCTCGTCAAGGGGCGGAGCTTATGGAAAAACG 5590

4271 AGTACTCACCAGTCAAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGCA 4330
|||||
2150 AGTACTCACCAGTCAAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGCA 2209
|||||
4331 GTGCTGCCATAACCAATAGTGTAAACACTGCGGCCAACTTACTTCTGCAACAGATCGGAG 4390
|||||
2210 GTGCTGCCATAACCAATAGTGTAAACACTGCGGCCAACTTACTTCTGCAACAGATCGGAG 2269
|||||
4391 GACCGAAGAGTAAACCGCTTTTGGCACAACATGGGGGATCATGTAACTCGCCTTGATC 4450
|||||
2270 GACCGAAGAGTAAACCGCTTTTGGCACAACATGGGGGATCATGTAACTCGCCTTGATC 2329
|||||
4451 GTTGGGAACCGAGCTGAATGAAGCATACCAACGAGCGGTGACACCAAGATGCGCTG 4510
|||||
2330 GTTGGGAACCGAGCTGAATGAAGCATACCAACGAGCGGTGACACCAAGATGCGCTG 2389
|||||
4511 TAGCAATGGCAACAACTGTTGCGCAAACTATTAACCTGGGGAATCTACTCTAGCTTCCC 4570
|||||
2390 TAGCAATGGCAACAACTGTTGCGCAAACTATTAACCTGGGGAATCTACTCTAGCTTCCC 2449
|||||
4571 GGCACAAATTAATAGACTGGATGGAGGGGATAAAGTTGCAGGACCACTTCTGCGCTGG 4630
|||||
2450 GGCACAAATTAATAGACTGGATGGAGGGGATAAAGTTGCAGGACCACTTCTGCGCTGG 2509
|||||
4631 CCTTCCGGCTGGCTGTTTATGTGATAAATCTGGAGCGGTGAGCGTGGTCTCGCG 4690
|||||
2510 CCTTCCGGCTGGCTGTTTATGTGATAAATCTGGAGCGGTGAGCGTGGTCTCGCG 2569
|||||
4691 GTATCAATTCAGACTGGGCGCAGATGGTAAAGCTCCCGTATCGTAGTTACTACAGA 4750
|||||
2570 GTATCAATTCAGACTGGGCGCAGATGGTAAAGCTCCCGTATCGTAGTTACTACAGA 2629
|||||
4751 CGGGAGTCAGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCTCTAC 4810
|||||
2630 CGGGAGTCAGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCTCTAC 2689
|||||
4811 TGATTAAGCATTTGTTAACTGTCAGACCAAGTTTACTCATATATCTTTAGATGATTAA 4870
|||||
2690 TGATTAAGCATTTGTTAACTGTCAGACCAAGTTTACTCATATATCTTTAGATGATTAA 2749
|||||
4871 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAATCTCATGACCA 4930
|||||
2750 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAATCTCATGACCA 2809
|||||
4931 AAATCCCTTAAGTCAAGTTTGTTCCTAGTGAAGCTGAGACCCGCTAGAAAAGATCAAG 4990
|||||
2810 AAATCCCTTAAGTCAAGTTTGTTCCTAGTGAAGCTGAGACCCGCTAGAAAAGATCAAG 2869
|||||
4991 GATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTTGTGCAAAACAAAACACAC 5050
|||||
2870 GATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTTGTGCAAAACAAAACACAC 2929
|||||
5051 CGCTACCAAGCGTGTGTTTGTTCGCGATCAAGAGCTACCAACTCTTTTCCGAAAGTAA 5110
|||||
2930 CGCTACCAAGCGTGTGTTTGTTCGCGATCAAGAGCTACCAACTCTTTTCCGAAAGTAA 2989
|||||
5111 CTGGCTTCAGACAGCGCAGATACCAATCTGCTTCTAGTGTAGCGGTAGTTAGGCC 5170
|||||
2990 CTGGCTTCAGACAGCGCAGATACCAATCTGCTTCTAGTGTAGCGGTAGTTAGGCC 3049
|||||
5171 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTTACCAG 5230
|||||
3050 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTTACCAG 3109
|||||
5231 TGGCTGCTGCCAGTGGCGATAGTCTGTTTACCGGGTTGGACTCAAGACGATAGTTAC 5290
|||||
3110 TGGCTGCTGCCAGTGGCGATAGTCTGTTTACCGGGTTGGACTCAAGACGATAGTTAC 3169
|||||
5291 CGGATAAGCGCAGCGCTGGCTGAAAGCGGGGTTCTGTCACACAGCCCGCTTGGAGC 5350
|||||
3170 CGGATAAGCGCAGCGCTGGCTGAAAGCGGGGTTCTGTCACACAGCCCGCTTGGAGC 3229
|||||
5351 GAAACGACCTACACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCGCCAGCTTC 5410
|||||

Db 3230 GAAACGACCTACACCGAATGAGATACCTACACGGTGAAGTATGAGAAAGCGCCACGCTTC 3289
|||||
QY 5411 CCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGGTCCGAAACAGGAGACGCA 5470
|||||
Db 3290 CCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGGTCCGAAACAGGAGACGCA 3349
|||||
QY 5471 CCGAGGAGCTTCCAGGGGGAAACCGCTGCTATCTTTATAGTCTGTCGGGTTTCGCCACC 5530
|||||
Db 3350 CCGAGGAGCTTCCAGGGGGAAACCGCTGCTATCTTTATAGTCTGTCGGGTTTCGCCACC 3409
|||||
QY 5531 TCTGACTTGAAGCGTCTGATTTTGTGATGCTCTGAGGGGGGAGCCCTATGAAAAACG 5590
|||||
Db 3410 TCTGACTTGAAGCGTCTGATTTTGTGATGCTCTGAGGGGGGAGCCCTATGAAAAACG 3469
|||||
QY 5591 CCAGCAACCGGCTTTTACGGTTCTCGGCTTTTGTGCGCTTTTGTCTACATGTTCT 5650
|||||
Db 3470 CCAGCAACCGGCTTTTACGGTTCTCGGCTTTTGTGCGCTTTTGTCTACATGTTCT 3529
|||||
QY 5651 TTCCTGGCTTATCCCTGATTTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATA 5710
|||||
Db 3530 TTCCTGGCTTATCCCTGATTTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATA 3589
|||||
QY 5711 CGCTCGCGCAGCGAAGCGACCGAGCGCAGCGAGTCACTGAGCGAGGAAGCGAAGAGC 5770
|||||
Db 3590 CGCTCGCGCAGCGAAGCGACCGAGCGCAGCGAGTCACTGAGCGAGGAAGCGAAGAGC 3649
|||||
QY 5771 GCCCAATACGCAACCGCTCTCCCGCGGCTGTCGCGATTCATTAATGCAG 5822
|||||
Db 3650 GCCCAATACGCAACCGCTCTCCCGCGGCTGTCGCGATTCATTAATGCAG 3701
|||||

RESULT 9

US-09-991-209-25
; sequence 25, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Philip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5277
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP5-1 vector
US-09-991-209-25

Query Match 47.5%; Score 2768; DB 10; Length 5277;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;
QY 2835 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTGCGGTC 2894
Db 894 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTGCGGTC 953
QY 2895 TTGGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACTGT 2954
Db 954 TTGGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACTGT 1013
QY 2955 AATCATGACGTTATTTATGAGATGGGTTTTTATGATTAGATCCCGCAATATACATTT 3014
Db 1014 AATCATGACGTTATTTATGAGATGGGTTTTTATGATTAGATCCCGCAATATACATTT 1073

QY	3015	AATACGGATAGAAAAAATAATAGCGCGCAAACTAGGATAAATTTATCGCGCGGTGT	3074	QY	4091	TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGATTTTCGCCGCCGAAG	4150
Db	1074	AATACGGATAGAAAAAATAATAGCGCGCAAACTAGGATAAATTTATCGCGCGGTGT	1133	Db	2086	TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGATTTTCGCCGCCGAAG	2145
QY	3075	CATCTATGTTACTAGATCGACCTCGACGCGATGGATCCGGCGCGCATGCGAGTCGGGC	3134	QY	4151	AAGCTTTTCAATGATGAGCACATTTTAAAGTTCTGCTATGTCGGCGGTATTTATCCCGTA	4210
Db	1134	CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGGTGGAGC-----T	1180	Db	2146	AAGCTTTTCAATGATGAGCACATTTTAAAGTTCTGCTATGTCGGCGGTATTTATCCCGTA	2205
QY	3135	CGAATTCGCCCTATAGTAGTGTGTAATAC-----AATTCACGTGGCGGTGTTTACAAAGTC	3191	QY	4211	TTGACGCGCGGCAAGAGCAACTCGGTCGCGCATACACTATTCTCAGAATGACTTGGTTG	4270
Db	1181	CGAATTCGCCCTATAGTAGTGTGTAATAC-----AATTCACGTGGCGGTGTTTACAAAGTC	1240	Db	2206	TTGACGCGCGGCAAGAGCAACTCGGTCGCGCATACACTATTCTCAGAATGACTTGGTTG	2265
QY	3192	GTGACTGGGAAAAACCTCGCGGTATACCAACTTAATCGCCTTGAAGCAATCCCGCTTTCG	3251	QY	4271	AGTACTCACCAATGATGAGCAATCTTACGGAATGCGATGACAGTAAAGAAATATGCA	4330
Db	1241	GTGACTGGGAAAAACCTCGCGGTATACCAACTTAATCGCCTTGAAGCAATCCCGCTTTCG	1300	Db	2266	AGTACTCACCAATGATGAGCAATCTTACGGAATGCGATGACAGTAAAGAAATATGCA	2325
QY	3252	CCAGCTGGCGTAATAGCAAGAGAGCCCGCACCGATCGCCCTTCCAAAGTGTGCGAGCC	3311	QY	4331	GTGCTGCCATAACCATGAGTGATAACACTCGGCGCAACTTACTTCTCACAACGATCGGAG	4390
Db	1301	CCAGCTGGCGTAATAGCAAGAGAGCCCGCACCGATCGCCCTTCCAAAGTGTGCGAGCC	1360	Db	2326	GTGCTGCCATAACCATGAGTGATAACACTCGGCGCAACTTACTTCTCACAACGATCGGAG	2385
QY	3312	TGATGCGGTAATAGCGCGCTGTAGCGCGCATTAAGCGCGCGGTGCTGGTGTGA	3370	QY	4391	GACCGAAGGAGCTAACCGCTTTTTTGGCAACAATGGGGGATCATGTAACTTGCCTTGTATC	4450
Db	1361	TGATGCGGTAATAGCGCGCTGTAGCGCGCATTAAGCGCGCGGTGCTGGTGTGA	1420	Db	2386	GACCGAAGGAGCTAACCGCTTTTTTGGCAACAATGGGGGATCATGTAACTTGCCTTGTATC	2445
QY	3371	CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCGCCCTTCCCTTTCCTTTC	3430	QY	4451	GTGCGAAGCGGAGCTGAATGAAGCCATACCAACAGAGCGGTGACACGATGCTG	4510
Db	1421	CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCGCCCTTCCCTTTCCTTTC	1480	Db	2446	GTGCGAAGCGGAGCTGAATGAAGCCATACCAACAGAGCGGTGACACGATGCTG	2505
QY	3431	CTTCCTTTTCGCGCACTGTCGCGCTTTCCCGTCAAGCTCTAAATTCGGGGGTCCCTT	3490	QY	4511	TAGCAATGGCAACAAACGCTGCGCAACTATTAACTGGCGCAACTTACTTCTAGCTTCCC	4570
Db	1481	CTTCCTTTTCGCGCACTGTCGCGCTTTCCCGTCAAGCTCTAAATTCGGGGGTCCCTT	1540	Db	2506	TAGCAATGGCAACAAACGCTGCGCAACTATTAACTGGCGCAACTTACTTCTAGCTTCCC	2565
QY	3491	TAGGTTCCGATTTAGAGCTTTACGACCTCGACCGCAAAACTTGATTTGGGTGATG	3550	QY	4571	GGCAACAATTAATAGATGGATGGAGCGGATTAAGTTGCAGGACCACTTCTGGGCTCGG	4630
Db	1541	TAGGTTCCGATTTAGAGCTTTACGACCTCGACCGCAAAACTTGATTTGGGTGATG	1600	Db	2566	GGCAACAATTAATAGATGGATGGAGCGGATTAAGTTGCAGGACCACTTCTGGGCTCGG	2625
QY	3551	GTTCACTGATGGGCGCATCGCCCTGATAGAGCGTTTTTCGCCCTTTCGAGCTGAGTCCA	3610	QY	4631	CCCTTCGCGCTGGCTGTTTATGCTGATTAATCTGGAGCGGTGAGCGGTGCTCGC	4690
Db	1601	GTTCACTGATGGGCGCATCGCCCTGATAGAGCGTTTTTCGCCCTTTCGAGCTGAGTCCA	1660	Db	2626	CCCTTCGCGCTGGCTGTTTATGCTGATTAATCTGGAGCGGTGAGCGGTGCTCGC	2685
QY	3611	CGTCTTTTAAATGATGGACTTTGTTCCAACTGGAACAACACTCAACCTATCTCGGTCT	3670	QY	4691	GTATCATGACGACTGGGCGGAGATGGTAAGCCCTCCGCTATCGTAGTTATCTACACGA	4750
Db	1661	CGTCTTTTAAATGATGGACTTTGTTCCAACTGGAACAACACTCAACCTATCTCGGTCT	1720	Db	2686	GTATCATGACGACTGGGCGGAGATGGTAAGCCCTCCGCTATCGTAGTTATCTACACGA	2745
QY	3671	ATTCCTTTGATTTAAGGATTTTTCGATTTTCGCTATTTGCTTAAATAATGAGCTGA	3730	QY	4751	CGGGAAGTACAGGCAACTATGGATCAACGAATAGACAGATCGCTGAGATAGTGCCTCAC	4810
Db	1721	ATTCCTTTGATTTAAGGATTTTTCGATTTTCGCTATTTGCTTAAATAATGAGCTGA	1780	Db	2746	CGGGAAGTACAGGCAACTATGGATCAACGAATAGACAGATCGCTGAGATAGTGCCTCAC	2805
QY	3731	TTTAAACAAATTTTAAACGCAATTTTAAACAAATTTTAAACGCTTTCGCTGATG	3790	QY	4811	TGATTAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTGATTAA	4870
Db	1781	TTTAAACAAATTTTAAACGCAATTTTAAACAAATTTTAAACGCTTTCGCTGATG	1831	Db	2806	TGATTAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTGATTAA	2865
QY	3791	CGGTAATTTTCTCCTTAACGCTATGTCGCTGATTTTCAACCGCATACAGGTGGCATTTTC	3850	QY	4871	AACCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGAATCTCTAGACCA	4930
Db	1832	CGGTAATTTTCTCCTTAACGCTATGTCGCTGATTTTCAACCGCATACAGGTGGCATTTTC	1845	Db	2866	AACCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGAATCTCTAGACCA	2925
QY	3851	GGGGAATGTCGGCGGACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGATC	3910	QY	4931	AAATCCCTTAACTGAGTGTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAAGTCAAG	4990
Db	1846	GGGGAATGTCGGCGGACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGATC	1905	Db	2926	AAATCCCTTAACTGAGTGTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAAGTCAAG	2985
QY	3911	CGCTCATGAGCAATAACCTGATAAATGCTTCAATATAATTTGAAAAAGGAGATGA	3970	QY	4991	GATCTTCTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTGCAACAAACCAAC	5050
Db	1906	CGCTCATGAGCAATAACCTGATAAATGCTTCAATATAATTTGAAAAAGGAGATGA	1965	Db	2986	GATCTTCTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTGCAACAAACCAAC	3045
QY	3971	GTAATTCACATTTCCGTGTCGCTTATTCCTTTTTTGGCGCATTTTGCCTTCTGTTT	4030	QY	5051	CGCTACAGCGGTGTTTGGTGGGATCAAGAGCTACCAACTCTTTTTCGAGGTAA	5110
Db	1966	GTAATTCACATTTCCGTGTCGCTTATTCCTTTTTTGGCGCATTTTGCCTTCTGTTT	2025	Db	3046	CGCTACAGCGGTGTTTGGTGGGATCAAGAGCTACCAACTCTTTTTCGAGGTAA	3105
QY	4031	TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG	4090	QY	5111	CTGCTTCTAGCAGCGCAGATACCAATACTGTCCTTCTAGTGTAGCGGTAGTGGCC	5170
Db	2026	TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG	2085	Db	3106	CTGCTTCTAGCAGCGCAGATACCAATACTGTCCTTCTAGTGTAGCGGTAGTGGCC	3165
				QY	5171	ACCACCTCAAGAACTCTGTAGCAGCGGCTACATACCTCGCTCTGCTAATCTGTTTACGAG	5230

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pIP4a2 vector
US-09-991-209-27

Query Match 47.5%; Score 2768; DB 10; Length 5327;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

```
QY 2835 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTCTTAAAGATTGAATCCTGTGCGCGTC 2894
Db 720 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTCTTAAAGATTGAATCCTGTGCGCGTC 779
QY 2895 TTGCGATGATTATCATATAATTTCTGTGAATAGTTTAAAGATTGAATCCTGTGCGCGTC 2954
Db 780 TTGCGATGATTATCATATAATTTCTGTGAATAGTTTAAAGATTGAATCCTGTGCGCGTC 839
QY 2955 AATGATGATGATTTATGAGATGGGTTTATGATTAGATCCCGCAATTAACATTT 3014
Db 840 AATGATGATGATTTATGAGATGGGTTTATGATTAGATCCCGCAATTAACATTT 899
QY 3015 AATGCGGATGAGAAAACAAATATAGCGCGCAAACTAGGATAAATATCGCGCGCGTGT 3074
Db 900 AATGCGGATGAGAAAACAAATATAGCGCGCAAACTAGGATAAATATCGCGCGCGTGT 959
QY 3075 CATCTATGTTACTAGATCGACCTGCGAGGATGGGATCCGCGCGCGCATGCGAGTCGGGC 3134
Db 960 CATCTATGTTACTAGATCGACCTGCGAGGATGGGATCCGCGCGCGCATGCGAGTCGGGC 1006
QY 3135 CCAATTCGCGCTATAGTACGTCGTATTAC---AATTACATGCGCGTCTGTTTACAAGTCT 3191
Db 1007 CCAATTCGCGCTATAGTACGTCGTATTACCGCGCTCACTGGCGCGTCTGTTTACAAGTCT 1066
QY 3192 GTGACTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCTTTCAGACACATCCCGCTTCG 3251
Db 1067 GTGACTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCTTTCAGACACATCCCGCTTCG 1126
QY 3252 CCAGCTGGCGTAAATAGCGAGAGCGCGACCGATCGCGCTTCCCAACAGTTGCGCAGCC 3311
Db 1127 CCAGCTGGCGTAAATAGCGAGAGCGCGACCGATCGCGCTTCCCAACAGTTGCGCAGCC 1186
QY 3312 TGAATGGCGAAT--GGACGCGCCCTGTAGCGGCGCATTAAGCGCGCGGTTGTTGTTA 1246
Db 1187 TGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGCGGTTGTTGTTA 1246
QY 3371 CGCGCAGCTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCCTTTCGCTTTCCTCC 3430
Db 1247 CGCGCAGCTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCCTTTCGCTTTCCTCC 1306
QY 3431 CTTCTCTTCTCGCAGTTTCGCGGTTTCCCGTCAAGCTCAATCCGGGGTCCCTT 3490
Db 1307 CTTCTCTTCTCGCAGTTTCGCGGTTTCCCGTCAAGCTCAATCCGGGGTCCCTT 1366
QY 3491 TAGGGTTCGATTTAGAGCTTTTACGCACTCGACGCGAAACCTGATTTGGGTGATG 3550
Db 1367 TAGGGTTCGATTTAGAGCTTTTACGCACTCGACGCGAAACCTGATTTGGGTGATG 1426
QY 3551 GTTACGTTAGTGGCCATCGCCCTGATAGAGCGTTTTCGCCCTTTGAGCTTGGAGTCCA 3610
Db 1427 GTTACGTTAGTGGCCATCGCCCTGATAGAGCGTTTTCGCCCTTTGAGCTTGGAGTCCA 1486
QY 3611 CGTTCTTTAATAGTGGACTCTGTTCCAAAATGGAACAACTCAACCTATCTCGGTCT 3670
Db 1487 CGTTCTTTAATAGTGGACTCTGTTCCAAAATGGAACAACTCAACCTATCTCGGTCT 1546
QY 3671 ATTCTTTTGAATTAAGGATTTTGGCGATTTGCGGCTATTGGTTAAATAATGAGCTGA 3730
Db 1547 ATTCTTTTGAATTAAGGATTTTGGCGATTTGCGGCTATTGGTTAAATAATGAGCTGA 1606
```

```
QY 3731 TTTACAATAATTTTAAACCGAATTTTAAACAAAATATTAAACGTTTACAATTTCCGCTGATG 3790
Db 1607 TTTACAATAATTTTAAACCGAATTTTAAACAAAATATTAAACGTTTACAATTT-----1657
QY 3791 CGGTATTTCTCTTACGCATCTGTGCGGTATTTCACACCGCATACAGTGGCACTTTTC 3850
Db 1658 -----AGTGGCACTTTTC1671
QY 3851 GGGGAAATGTGCGGGAACCCCTATTGTTTATTATTTTCTAAATACTTCAAAATATGATC 3910
Db 1672 GGGGAAATGTGCGGGAACCCCTATTGTTTATTATTTTCTAAATACTTCAAAATATGATC 1731
QY 3911 CGCTCATGAGACAATAACCTGTAAATGCTTCAATAATATTGAAAAAGAGAGTATGA 3970
Db 1732 CGCTCATGAGACAATAACCTGTAAATGCTTCAATAATATTGAAAAAGAGAGTATGA 1791
QY 3971 GTATTCAACATTTCCGTGTGCGCCCTTATCCCTTTTGGGCAATTTGCGCTCTCTGTTT 4030
Db 1792 GTATTCAACATTTCCGTGTGCGCCCTTATCCCTTTTGGGCAATTTGCGCTCTCTGTTT 1851
QY 4031 TTGCTCAACCGAAGAACCGCTGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 4090
Db 1852 TTGCTCAACCGAAGAACCGCTGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 1911
QY 4091 TGGGTTACATCGAATCGATCTCAACAGCGGTGAAGTCTCTTGAGAGTTTTCGCCCGAAG 4150
Db 1912 TGGGTTACATCGAATCGATCTCAACAGCGGTGAAGTCTCTTGAGAGTTTTCGCCCGAAG 1971
QY 4151 AACGTTTTCCTCAATGATGAGCACTTTTAAAGTCTCTGCTATGTTGGCGCGTATTATCCCGTA 4210
Db 1972 AACGTTTTCCTCAATGATGAGCACTTTTAAAGTCTCTGCTATGTTGGCGCGTATTATCCCGTA 2031
QY 4211 TTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAAGTCTGTTG 4270
Db 2032 TTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAAGTCTGTTG 2091
QY 4271 AGTACTCACGAGTCAAGAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATATGCA 4330
Db 2092 AGTACTCACGAGTCAAGAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATATGCA 2151
QY 4331 GTGCTGCCATAACCATGAGTGAATACTGCGGCAACTTCTTCTGCAACAGATCGGAG 4390
Db 2152 GTGCTGCCATAACCATGAGTGAATACTGCGGCAACTTCTTCTGCAACAGATCGGAG 2211
QY 4391 GACCGAAGAGCTAACCGCTTTTTCACAAACATGGGGATCATGTAATCGCTTGTATC 4450
Db 2212 GACCGAAGAGCTAACCGCTTTTTCACAAACATGGGGATCATGTAATCGCTTGTATC 2271
QY 4451 GTTGGGACCGGAGCTGAATGAAGCATACAAAACGACGAGCGTGACACCGATCGCTG 4510
Db 2272 GTTGGGACCGGAGCTGAATGAAGCATACAAAACGACGAGCGTGACACCGATCGCTG 2331
QY 4511 TAGCAATGCAACAACTGTTGGCAACTATTAACTGGCGAACTACTTACTTAGCTTCC 4570
Db 2332 TAGCAATGCAACAACTGTTGGCAACTATTAACTGGCGAACTACTTACTTAGCTTCC 2391
QY 4571 GGCACAAATTAATAGACTGGATGGAGCGGATAAAGTTGACGACCACTTCTGCGCTCGG 4630
Db 2392 GGCACAAATTAATAGACTGGATGGAGCGGATAAAGTTGACGACCACTTCTGCGCTCGG 2451
QY 4631 CCCTTCCGCTGGCTGGTTTATGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGG 4690
Db 2452 CCCTTCCGCTGGCTGGTTTATGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGG 2511
QY 4691 GTATCATTTGACGACTGGGCGCAGATGTAAGCCCTCCGTTATCGTAGTTATCTACAGA 4750
Db 2512 GTATCATTTGACGACTGGGCGCAGATGTAAGCCCTCCGTTATCGTAGTTATCTACAGA 2571
QY 4751 CGGGAGTTCAGGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTCTCTCAC 4810
Db 2572 CGGGAGTTCAGGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTCTCTCAC 2631
QY 4811 TGATTAAGCATTTGTAATCTGACAGCAAGTTTACTCATATATATCTTAGATTGATTAA 4870
```

Db	2632	TGATTAAGCATTTGGTAAGTGTGACCAAGTTTACTCATATATCTTATGATGATTAA	2691
Qy	4871	AACTTCATTTTAAATTTAAAGGATCTAGGTAAGATCTCTTTTGAATACTCATGACCA	4930
Db	2692	AACTTCATTTTAAATTTAAAGGATCTAGGTAAGATCTCTTTTGAATACTCATGACCA	2751
Qy	4931	AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAG	4990
Db	2752	AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAG	2811
Qy	4991	GATCTCTTGAGATCTCTTTTCTGCGGTAATCTGCTGTGCAACAAAAAACAC	5050
Db	2812	GATCTCTTGAGATCTCTTTTCTGCGGTAATCTGCTGTGCAACAAAAAACAC	2871
Qy	5051	CGTACCAAGCGGTGGTTTGGCGGATCAAGAGTACCACTCTTTTTCGGAAGTAA	5110
Db	2872	CGTACCAAGCGGTGGTTTGGCGGATCAAGAGTACCACTCTTTTTCGGAAGTAA	2931
Qy	5111	CTGGCTTCAGCAGCGCAGATACCAATATCTGCTCTCTAGTGTAGCGGTAGTAGGCC	5170
Db	2932	CTGGCTTCAGCAGCGCAGATACCAATATCTGCTCTCTAGTGTAGCGGTAGTAGGCC	2991
Qy	5171	ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTCTGTACAG	5230
Db	2992	ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTCTGTACAG	3051
Qy	5231	TGGCTGTGCCAGTGGCGAATAGTGTGTCTTACCGGGTGTGACTCAAGACATAGTTAC	5290
Db	3052	TGGCTGTGCCAGTGGCGAATAGTGTGTCTTACCGGGTGTGACTCAAGACATAGTTAC	3111
Qy	5291	CGGATAAGCGCAGCGGTGGGCTGAAACGGGGGTTCGTGACACAGCCCGCTGGAGC	5350
Db	3112	CGGATAAGCGCAGCGGTGGGCTGAAACGGGGGTTCGTGACACAGCCCGCTGGAGC	3171
Qy	5351	GAACGACCTTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAACGCCACGCTTC	5410
Db	3172	GAACGACCTTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAACGCCACGCTTC	3231
Qy	5411	CCGAAAGGAGAAAGCGCGACAGGTATCCGGTAAAGCGGAGGTCGGAACAGGAGCGCA	5470
Db	3232	CCGAAAGGAGAAAGCGCGACAGGTATCCGGTAAAGCGGAGGTCGGAACAGGAGCGCA	3291
Qy	5471	CGAGGAGCTTCCAGGGGAAACCGCTGATCTTTATAGTCTCTGCGGTTTCGCCACC	5530
Db	3292	CGAGGAGCTTCCAGGGGAAACCGCTGATCTTTATAGTCTCTGCGGTTTCGCCACC	3351
Qy	5531	TCTGACTTGACGCTCGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTATGAAAAACG	5590
Db	3352	TCTGACTTGACGCTCGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTATGAAAAACG	3411
Qy	5591	CCAGCAACCGCGCTTTTACGGTTCTTGCCCTTTTGTGCTGCTTTCACATGTTCT	5650
Db	3412	CCAGCAACCGCGCTTTTACGGTTCTTGCCCTTTTGTGCTGCTTTCACATGTTCT	3471
Qy	5651	TTCTCTGCTTATCCCTGATCTCTGATTAACGCTATTACCGCTTTGATGAGCTGATA	5710
Db	3472	TTCTCTGCTTATCCCTGATCTCTGATTAACGCTATTACCGCTTTGATGAGCTGATA	3531
Qy	5711	CCGCTCCCGCAGCCGAAACCGAGCGCAGCGAGTCAGTGAGCGAGAAACGAGC	5770
Db	3532	CCGCTCCCGCAGCCGAAACCGAGCGCAGCGAGTCAGTGAGCGAGAAACGAGC	3591
Qy	5771	GCCCAATACGAAACCGCTCTCCCGCGGCTTGGCGGATTCATTATGCGAG	5822
Db	3592	GCCCAATACGAAACCGCTCTCCCGCGGCTTGGCGGATTCATTATGCGAG	3643

Query Match 47.5%; Score 2768; DB 10; Length 5337;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCAACAAATTTGGCAATAAAGTTTCTTAAGATTGAATCTGTGCGGTC 2894
Db 954 AAGCAGATCGTTCAACAAATTTGGCAATAAAGTTTCTTAAGATTGAATCTGTGCGGTC 1013
Qy 2895 TTGCGATGATTATATATAATTTCTGTGTAATTAAGCATGTAATAATTAACATGT 2954
Db 1014 TTGCGATGATTATATATAATTTCTGTGTAATTAAGCATGTAATAATTAACATGT 1073
Qy 2955 AATGCATGACGTTATTTATAGATCGGTTTATGATAGATCCCGCAATATATACATTT 3014
Db 1074 AATGCATGACGTTATTTATGATCGGTTTATGATAGATCCCGCAATATATACATTT 1133
Qy 3015 AATAGCGATAGAAACAAATATAGCGGCAAACTAGGATAAAATTTATCGCGCGGTGT 3074
Db 1134 AATAGCGATAGAAACAAATATAGCGGCAAACTAGGATAAAATTTATCGCGCGGTGT 1193
Qy 3075 CATCTATGTTACTAGATCGACCTGAGGATCGGATCCGCGCGCATCGAGCTCGGGC 3134
Db 1194 CATCTATGTTACTAGATCGATTAAGCTTCTAGAGCGCGGTGGAGC-----T 1240
Qy 3135 CCAATTCGCCCTATAGTGTAGTGTATAC-----AATTCATGCGCGCTGTTTACAGCTC 3191
Db 1241 CCAATTCGCCCTATAGTGTAGTGTATAC-----AATTCATGCGCGCTGTTTACAGCTC 1300
Qy 3192 GTGACTGGGAAACCCCTGGGTTTACCACTTAATCGCTTGCAGCACATCCGCCCTTCG 3251
Db 1301 GTGACTGGGAAACCCCTGGGTTTACCACTTAATCGCTTGCAGCACATCCGCCCTTCG 1360
Qy 3252 CCAGCTGGGCTTAATAGCGAAGAGCGCGCACCGATCGCTTCCCAACAGTTGCGCAGCC 3311
Db 1361 CCAGCTGGGCTTAATAGCGAAGAGCGCGCACCGATCGCTTCCCAACAGTTGCGCAGCC 1420
Qy 3312 TGAATGCGCAAT--GGAGCGCCCTGTAGCGGCGCATTAAGCGGCGGTTGTGTGGTTA 3370
Db 1421 TGAATGCGCAAT--GGAGCGCCCTGTAGCGGCGCATTAAGCGGCGGTTGTGTGGTTA 1480
Qy 3371 CGGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCGCTTCCCTTTCCTTCCTCC 3430
Db 1481 CGGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCGCTTCCCTTTCCTTCCTCC 1540
Qy 3431 CTTCTCTTCTCGCCACCGTTTCGCCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTT 3490
Db 1541 CTTCTCTTCTCGCCACCGTTTCGCCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTT 1600
Qy 3491 TAGGTTCCGATTTAGAGCTTTAGCGACCTCGACCGCAAAACTTGAATTTGGTGATG 3550
Db 1601 TAGGTTCCGATTTAGTGTCTTTACGGCACCTTCGACCCCAAAACTTGAATTTGGTGATG 1660

APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Langdon, Timothy
APPLICANT: Morse, Phillip
TITLE OF INVENTION: Manipulation of the Phenolic Acid
TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
FILE REFERENCE: GC648-2
CURRENT APPLICATION NUMBER: US/09/991,209
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/249,608
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 5337
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pTU4 vector
US-09-991-209-19

QY	3551	GTTCAGT	AGTGGG	CCATCGCC	TGATAGACGG	TTTTTCGGC	TTTGTAGAGTTGGAGTCCA	3610
Db	1661	GTTCAGT	AGTGGG	CCATCGCC	TGATAGACGG	TTTTTCGGC	TTTGTAGAGTTGGAGTCCA	1720
QY	3611	CGTCTCTT	TAATAGTGG	ACTCTGTTC	CCAACTGG	GAACAAC	ACTCAACCTTATCTCGGTCT	3670
Db	1721	CGTCTCTT	TAATAGTGG	ACTCTGTTC	CCAACTGG	GAACAAC	ACTCAACCTTATCTCGGTCT	1780
QY	3671	ATTCTTTT	GATTTAAG	GGGATTTT	CGCGATTT	CGGCCTAT	TGGTTAAAAAATGAGCTGA	3730
Db	1781	ATTCTTTT	GATTTAAG	GGGATTTT	CGCGATTT	CGGCCTAT	TGGTTAAAAAATGAGCTGA	1840
QY	3731	TTTAA	CAAAATTTTAA	CGGGAATTTT	TAA	CAAAATTTTAA	CGGCTTTCGCTGATG	3790
Db	1841	TTTAA	CAAAATTTTAA	CGGGAATTTT	TAA	CAAAATTTTAA	CGGCTTTCGCTGATG	3790
QY	3791	CGGTATTT	CTCCTT	TAAGCA	CTCTG	CGCGTATTT	CACACCGCATACAGTGGCGACTTTTC	3850
Db	1892	-----	-----	-----	-----	-----	AGGTGGCACTTTTC	1905
QY	3851	GGG	GAATGTGCGG	GAACCC	CTATTTT	CTATTTTCT	AAATACATTTCAATATGATC	3910
Db	1906	GGG	GAATGTGCGG	GAACCC	CTATTTT	CTATTTTCT	AAATACATTTCAATATGATC	1965
QY	3911	CGCTCAT	GAGCAAT	TAACCT	TGATAAT	GTCTCAAT	TAATTTGAAAAGGAAGATGA	3970
Db	1966	CGCTCAT	GAGCAAT	TAACCT	TGATAAT	GTCTCAAT	TAATTTGAAAAGGAAGATGA	2025
QY	3971	GTATT	CAACATTT	CGGTG	CGCCCTTAT	TCCTTTT	TGGGCATTTTGGCTTCCTGTTT	4030
Db	2026	GTATT	CAACATTT	CGGTG	CGCCCTTAT	TCCTTTT	TGGGCATTTTGGCTTCCTGTTT	2085
QY	4031	TTGCT	CA	CCGA	AAACGCTGGT	GAAGTCTGAAG	ATCAGTCGGTGCACGAG	4090
Db	2086	TTGCT	CA	CCGA	AAACGCTGGT	GAAGTCTGAAG	ATCAGTCGGTGCACGAG	2145
QY	4091	TGG	GTATCAT	GAAC	CTGGA	CTCAACAG	CGGTGAAGATCTTTTCGCCCGAAG	4150
Db	2146	TGG	GTATCAT	GAAC	CTGGA	CTCAACAG	CGGTGAAGATCTTTTCGCCCGAAG	2205
QY	4151	AAC	GTTTTTCA	ATCAT	GAGCACTTTT	AAAGTCTGCT	ATGTCGGCGGATTTATCCGTTA	4210
Db	2206	AAC	GTTTTTCA	ATCAT	GAGCACTTTT	AAAGTCTGCT	ATGTCGGCGGATTTATCCGTTA	2265
QY	4211	TTG	ACGCGG	CGAAGAG	CAACTCG	GTCCGCGCATACACT	ATTCTCAGATGACTTCGTTG	4270
Db	2266	TTG	ACGCGG	CGAAGAG	CAACTCG	GTCCGCGCATACACT	ATTCTCAGATGACTTCGTTG	2325
QY	4271	AGT	ACTC	ACAGT	CACAGAAAG	CACTTTAC	GGATGGCATGACAGTAAGAAATTATGA	4330
Db	2326	AGT	ACTC	ACAGT	CACAGAAAG	CACTTTAC	GGATGGCATGACAGTAAGAAATTATGA	2385
QY	4331	GTG	CTGCC	ATAACCAT	GAGTGATAAC	ACTCGCGCC	CAACTTCTTGCAACGATCGGAG	4390
Db	2386	GTG	CTGCC	ATAACCAT	GAGTGATAAC	ACTCGCGCC	CAACTTCTTGCAACGATCGGAG	2445
QY	4391	GAC	CGAAG	GAGCTTAA	CCGCTTTTTT	TGCACAA	CAATGGGGCATGATGAACTCGCTTTGATC	4450
Db	2446	GAC	CGAAG	GAGCTTAA	CCGCTTTTTT	TGCACAA	CAATGGGGCATGATGAACTCGCTTTGATC	2505
QY	4451	GT	TGGNA	CCG	GAGCTGAATGA	AGCATA	CCAAACGACGAGGTGACACGATGCCTG	4510
Db	2506	GT	TGGNA	CCG	GAGCTGAATGA	AGCATA	CCAAACGACGAGGTGACACGATGCCTG	2565
QY	4511	TAG	CAAT	TGG	CAACAA	CGTTGCG	CAAACTTAACTGGCGAACTACTTACTTAGCTTCCC	4570
Db	2566	TAG	CAAT	TGG	CAACAA	CGTTGCG	CAAACTTAACTGGCGAACTACTTACTTAGCTTCCC	2625
QY	4571	GG	CAACAA	TTAATAG	ACTTGA	TGGAGCGG	GAATAAGTTTCAGAGCACTTCTCGCTCGG	4630
Db	2626	GG	CAACAA	TTAATAG	ACTTGA	TGGAGCGG	GAATAAGTTTCAGAGCACTTCTCGCTCGG	2685
QY	4631	CC	TTCCG	CTG	CGTGGTTT	TGTTG	TGTAFAAATCTGGAGCCGGTGAGGTGGGTCTCGC	4690

Db	2686	CCCTTCGGCTGGCTGGTTTATTCGTGATAAATCTGGAGCGGTGACGCTGGGTCTCGCG	2745
QY	4691	GTATCAATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCTGTAAGTTATCTACACGA	4750
Db	2746	GTATCAATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCTGTAAGTTATCTACACGA	2805
QY	4751	CGGGAGTCAGCAACTATGATGAACGAATAGACAGATCGTGTGAGATAGGTGCCTCAC	4810
Db	2806	CGGGAGTCAGCAACTATGATGAACGAATAGACAGATCGTGTGAGATAGGTGCCTCAC	2865
QY	4811	TGATTAAGCATTTGGTTAACTGTCACAGCAAGTTTACTCATATATACITTTAGATTGATTAA	4870
Db	2866	TGATTAAGCATTTGGTTAACTGTCACAGCAAGTTTACTCATATATACITTTAGATTGATTAA	2925
QY	4871	AACITCAITTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATCACCA	4930
Db	2926	AACITCAITTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATCACCA	2985
QY	4931	AAATCCCTTAACGTGAGTTTTCGTTTCACTGAGGGTCAGACCCGCTAGAAAAAGATCAAA	4990
Db	2986	AAATCCCTTAACGTGAGTTTTCGTTTCACTGAGGGTCAGACCCGCTAGAAAAAGATCAAA	3045
QY	4991	GATCTTCTTGAGATCCCTTTTCTCGCGCGTAATCTGCTGCTTGCAAAACAAAAAACCA	5050
Db	3046	GATCTTCTTGAGATCCCTTTTCTCGCGCGTAATCTGCTGCTTGCAAAACAAAAAACCA	3105
QY	5051	CGCTACACGCGGTGGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAA	5110
Db	3106	CGCTACACGCGGTGGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTCCGAAGGTAA	3165
QY	5111	CTGCGTTACGAGAGCGCAGATACCAAAATCTGCTCTTAGTGTAGCGGTAGTTAGGCC	5170
Db	3166	CTGCGTTACGAGAGCGCAGATACCAAAATCTGCTCTTAGTGTAGCGGTAGTTAGGCC	3225
QY	5171	ACCACTTCAAGAACTCTGTAGACACCGCTACATACCTCGCTCTGTAATCTCTGTACAG	5230
Db	3226	ACCACTTCAAGAACTCTGTAGACACCGCTACATACCTCGCTCTGTAATCTCTGTACAG	3285
QY	5231	TGGCTGTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGACCTCAAGACGATAGTTAC	5290
Db	3286	TGGCTGTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGACCTCAAGACGATAGTTAC	3345
QY	5291	CGGNTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTGCACAAGCCACGTTGGAGC	5350
Db	3346	CGGNTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTGCACAAGCCACGTTGGAGC	3405
QY	5351	GAACGACCTACACCGAACTGAGATACCTACAGGTGAGCTATGAAAGCGCCAGCTTC	5410
Db	3406	GAACGACCTACACCGAACTGAGATACCTACAGGTGAGCTATGAAAGCGCCAGCTTC	3465
QY	5411	CCGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGCGCAGGGTCCGAAACGAGAGCGCA	5470
Db	3466	CCGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGCGCAGGGTCCGAAACGAGAGCGCA	3525
QY	5471	CGAGGAGCTTCCAGGGGAAACGCTCGTATCTTTATAGTCTGTGCGGTTTCGCCACC	5530
Db	3526	CGAGGAGCTTCCAGGGGAAACGCTCGTATCTTTATAGTCTGTGCGGTTTCGCCACC	3585
QY	5531	CTGACTTCAGCGCTCGATTTTGTGATGCTCGTCAGGGGGCGAGCCTATGGAAGAACG	5590
Db	3586	CTGACTTCAGCGCTCGATTTTGTGATGCTCGTCAGGGGGCGAGCCTATGGAAGAACG	3645
QY	5591	CCAGCAACCGGCTTTTATCGGTTCCCTGGCCTTTTGTGCGCCTTTTGTCTACATGTCT	5650
Db	3646	CCAGCAACCGGCTTTTATCGGTTCCCTGGCCTTTTGTGCGCCTTTTGTCTACATGTCT	3705
QY	5651	TTCTTCGCTTATCCCTGATTCTGTGGAATAACCGTATTAACCGCCTTTTGTGTGAGCTGATA	5710
Db	3706	TTCTTCGCTTATCCCTGATTCTGTGGAATAACCGTATTAACCGCCTTTTGTGTGAGCTGATA	3765
QY	5711	CGCTCGCGCAGCGCAACGACCGAGCGCAGCTCAGTGTGCGCAGCAAGCGGAGAGGC	5770

Db 3766 CCGCTCCGCGAGCGAAGCAGCGAGCGAGTCACTGAGCGAGGAGCGAAGAGAGC 3825
Qy 5771 GCCCAATACGAAACCGCTCTCCCGCGGCGTGGCGGATTCATTAATGCAG 5822
Db 3826 GCCCAATACGAAACCGCTCTCCCGCGGCGTGGCGGATTCATTAATGCAG 3877

RESULT 13
US-09-991-209-23
; Sequence 23, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 5337
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP8-5 vector
US-09-991-209-23

Query Match 47.5%; Score 2768; DB 10; Length 5337;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCACACATTTGCGCAATTAAGTTCTTAAGATTGAATCCGTGCGCGTC 2894
Db 954 AAGCAGATCGTTCACACATTTGCGCAATTAAGTTCTTAAGATTGAATCCGTGCGCGTC 1013
Qy 2895 TTGCGATGATTAATCATATAATTTCTGTTGAATTAAGTAAAGTAAATTAATTAATGAT 2954
Db 1014 TTGCGATGATTAATCATATAATTTCTGTTGAATTAAGTAAAGTAAATTAATTAATGAT 1073
Qy 2955 AATGCAATGATTAATTAAGATGGTCTTATGATTAAGTAAAGTAAATTAATTAATTAATGAT 3014
Db 1074 AATGCAATGATTAATTAAGATGGTCTTATGATTAAGTAAAGTAAATTAATTAATTAATGAT 1133
Qy 3015 AATACGCGATAGAAACAAATATAGCGCAAACTAGGATAAATTAATTAATTAATTAATTAATGAT 3074
Db 1134 AATACGCGATAGAAACAAATATAGCGCAAACTAGGATAAATTAATTAATTAATTAATTAATGAT 1193
Qy 3075 CATCTATGTTACTAGATCGACCTGCGGATGGATCCGCGCGCGATGAGCGTGGGC 3134
Db 1194 CATCTATGTTACTAGATCGATAGCTTCTAGCGCGCGGTGGAGC-----T 1240
Qy 3135 CCAATTCGCCCTATAGTAGTGTATTTAC---AATTCACGTGCGGTGTTTACACGTC 3191
Db 1241 CCAATTCGCCCTATAGTAGTGTATTTACCGCGCTCCTGCGCGCTGTTTACACGTC 1300
Qy 3192 GTGACTGGGAAACCCCTGGCGTTTACCCTAATTCGCCCTTGCAGCATCCCGCTTCG 3251
Db 1301 GTGACTGGGAAACCCCTGGCGTTTACCCTAATTCGCCCTTGCAGCATCCCGCTTCG 1360
Qy 3252 CCAGCTGGCGTAAATAGCGAAGAGCGCCGCGATGCGGCTTCCCAACAGTTGGCGAGCC 3311
Db 1361 CCAGCTGGCGTAAATAGCGAAGAGCGCCGCGATGCGGCTTCCCAACAGTTGGCGAGCC 1420
Qy 3312 TGAATGCGGAT--GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTGA 3370
Db 1421 TGAATGCGGATGGAACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTGA 1480

Qy 3371 CGCGCAGGTGACCGCTACACTTCCGAGCGCCCTAGCGCGCTCTTTCGCTTCTTCC 3430
Db 1481 CGCGCAGGTGACCGCTACACTTCCGAGCGCCCTAGCGCGCTCTTTCGCTTCTTCC 1540
Qy 3431 CTTCTCTTTCGCGCAGCTTCCCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTTCCCTT 3490
Db 1541 CTTCTCTTTCGCGCAGCTTCCCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTTCCCTT 1600
Qy 3491 TAGGGTTCCGATTTAGAGCTTTACGGCACCTCGGACCGGCAAAATCTTGAATTTGGGTGATG 3550
Db 1601 TAGGGTTCCGATTTAGTGTCTTACGGCACCTCGGACCGGCAAAATCTTGAATTTGGGTGATG 1660
Qy 3551 GTTCACTAGTGGGCGCATCGGCTGATAGAGCGGTTTTTCGCGCTTTCGAGTTCAGTCA 3610
Db 1661 GTTCACTAGTGGGCGCATCGGCTGATAGAGCGGTTTTTCGCGCTTTCGAGTTCAGTCA 1720
Qy 3611 CGTCTTTTAAATAGTGGACTCTTGTTCGAACTGGAACCAACTCAACCTATCTCGGTCT 3670
Db 1721 CGTCTTTTAAATAGTGGACTCTTGTTCGAACTGGAACCAACTCAACCTATCTCGGTCT 1780
Qy 3671 ATTCTTTTGAATTTAAGGGAATTTTCGCGATTTTCGCGCTTTCGTTTAAATAGTCA 3730
Db 1781 ATTCTTTTGAATTTAAGGGAATTTTCGCGATTTTCGCGCTTTCGTTTAAATAGTCA 1840
Qy 3731 TTTAAACAATATTTAAACGCGAATTTTAAACAATATTTAAACAATTTTCGCGCTGATG 3790
Db 1841 TTTAAACAATATTTAAACGCGAATTTTAAACAATATTTAAACAATTTTCGCGCTGATG 1891
Qy 3791 CGGTATTTTCTCTTACGCACTCTGTGCGGTATTTTACACCGCATACAGTGCACCTTTTC 3850
Db 1892 -----AGTGGCACTTTTC 1905
Qy 3851 GGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGTATC 3910
Db 1906 GGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGTATC 1965
Qy 3911 CGCTCATGAGACAATAACCTGATTAATGCTTCAATAATTTGAAAGAGAGAGATGATGA 3970
Db 1966 CGCTCATGAGACAATAACCTGATTAATGCTTCAATAATTTGAAAGAGAGAGATGATGA 2025
Qy 3971 GTATTCACATTTCCGTGTCGCGCTTATTTCCCTTTTTCGCGCATTTTTCCTTCTGTTT 4030
Db 2026 GTATTCACATTTCCGTGTCGCGCTTATTTCCCTTTTTCGCGCATTTTTCCTTCTGTTT 2085
Qy 4031 TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATCTGAAGATCAGTTGGGTGCGAGG 4090
Db 2086 TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATCTGAAGATCAGTTGGGTGCGAGG 2145
Qy 4091 TGGGTTTACATCGAATCGGATCTCAACAGCGGTAAGATCTTGAAGAGTTTTCGCGCGGAAG 4150
Db 2146 TGGGTTTACATCGAATCGGATCTCAACAGCGGTAAGATCTTGAAGAGTTTTCGCGCGGAAG 2205
Qy 4151 AAGCTTTTCCAAATGATGAGCATTTTAAAGTTCTGCTATGTGCGCGGTATTTATTCGGTA 4210
Db 2206 AAGCTTTTCCAAATGATGAGCATTTTAAAGTTCTGCTATGTGCGCGGTATTTATTCGGTA 2265
Qy 4211 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGATACACTATTTCTCAGAATGACTGTTG 4270
Db 2266 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGATACACTATTTCTCAGAATGACTGTTG 2325
Qy 4271 AGTACTCACAGTACAGAAAGCACTTACCGATGGCATGACAGTAAGAGAAATATGCA 4330
Db 2326 AGTACTCACAGTACAGAAAGCACTTACCGATGGCATGACAGTAAGAGAAATATGCA 2385
Qy 4331 GTGCTGCCATAAACCATGAGTGAATAACACTCGCGCAACTTACTTCTGACAAAGATCGAG 4390
Db 2386 GTGCTGCCATAAACCATGAGTGAATAACACTCGCGCAACTTACTTCTGACAAAGATCGAG 2445
Qy 4391 GACCGAAGAGAGTAAACCGCTTTTTCGCAACATGGGGGATCATGTAACCTCGCTTGCATC 4450
Db 2446 GACCGAAGAGAGTAAACCGCTTTTTCGCAACATGGGGGATCATGTAACCTCGCTTGCATC 2505
Qy 4451 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGCGGTGACACCAAGATGCTG 4510

Db	2506	GTITGGGAACCGGAGCTGANTGAAGCCATACCAACGACGAGCGTGAACACACGATGGCTG	2565
QY	4511	TAGCAATGGCAACAACGTTTGGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCC	4570
Db	2566	TAGCAATGGCAACAACGTTTGGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCC	2625
QY	4571	GGCAACAATTAATAGACTGCGATGGAGGGCGGATAAAGTTGACAGCACTCTTGGCGTCGG	4630
Db	2626	GGCAACAATTAATAGACTGCGATGGAGGGCGGATAAAGTTGACAGCACTCTTGGCGTCGG	2685
QY	4631	CCCTTCCGCGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGACGTTGGCTCTCGCG	4690
Db	2686	CCCTTCCGCGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGACGTTGGCTCTCGCG	2745
QY	4691	GTATCATTTGCACACTGCGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTTATCTACACGA	4750
Db	2746	GTATCATTTGCACACTGCGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTTATCTACACGA	2805
QY	4751	CGGGAGCTCAGCAACTATGATGAAAGAAATAGACAGATCGCTGAGTAGTGCCTCAC	4810
Db	2806	CGGGAGCTCAGCAACTATGATGAAAGAAATAGACAGATCGCTGAGTAGTGCCTCAC	2865
QY	4811	TGATTAAGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATACITTAGATTGATTTAA	4870
Db	2866	TGATTAAGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATACITTAGATTGATTTAA	2925
QY	4871	AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATATCTCATGACCA	4930
Db	2926	AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATATCTCATGACCA	2985
QY	4931	AAATCCCTTAACGTAGTTTTTCTGCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAG	4990
Db	2986	AAATCCCTTAACGTAGTTTTTCTGCTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAG	3045
QY	4991	GATCTTCTTGAGATCCCTTTTCTGCGCGTAACTCTGCTGTCGCAAAACAAAAACCAAC	5050
Db	3046	GATCTTCTTGAGATCCCTTTTCTGCGCGTAACTCTGCTGTCGCAAAACAAAAACCAAC	3105
QY	5051	CGCTACCAAGCGGTGGTTTGTTCGGGATCAAGAGCTACCACTCTTTTCCGAGGTAA	5110
Db	3106	CGCTACCAAGCGGTGGTTTGTTCGGGATCAAGAGCTACCACTCTTTTCCGAGGTAA	3165
QY	5111	CTGCGTTTCAGAGCGCAGATACCAAACTCTCCTTCTAGTGTAGCGGTAGTTAGGCC	5170
Db	3166	CTGCGTTTCAGAGCGCAGATACCAAACTCTCCTTCTAGTGTAGCGGTAGTTAGGCC	3225
QY	5171	ACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTGCTAAATCCTGTGTACCAG	5230
Db	3226	ACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTGCTAAATCCTGTGTACCAG	3285
QY	5231	TGGTGCTGCGACGTGGCGGATAAGTCTGTCTTACCGGTTGACCTCAAGACGATGTAC	5290
Db	3286	TGGTGCTGCGACGTGGCGGATAAGTCTGTCTTACCGGTTGACCTCAAGACGATGTAC	3345
QY	5291	CGGATAAGCGCAGCGGTGGGTGAAACGGGGGGTTCTGTGACAGCCCGAGCTTGGAGC	5350
Db	3346	CGGATAAGCGCAGCGGTGGGTGAAACGGGGGGTTCTGTGACAGCCCGAGCTTGGAGC	3405
QY	5351	GAACGACCTTACCGCAACTGAGATACCTACACGCTGAGCTATGAGAAAGCCCGCTTC	5410
Db	3406	GAACGACCTTACCGCAACTGAGATACCTACACGCTGAGCTATGAGAAAGCCCGCTTC	3465
QY	5411	CCGAAGGGGAAAGCGGACAGGTATCCGGTAAGCGCGGAGGTCCGAACAGGAGCGCA	5470
Db	3466	CCGAAGGGGAAAGCGGACAGGTATCCGGTAAGCGCGGAGGTCCGAACAGGAGCGCA	3525
QY	5471	CGAGGAGCTTCCAGGGGAAACGGCTGTATCTTTATAGTCTCTGCTGGGTTTCGCCACC	5530
Db	3526	CGAGGAGCTTCCAGGGGAAACGGCTGTATCTTTATAGTCTCTGCTGGGTTTCGCCACC	3585
QY	5531	TCTGACTTTCAGCGTCAATTTTTTGTGATGCTGCTCAGGGGGCGGAGCTATGGAATAACG	5590

Db 3586 TCTGACTTTGAGCGTTCGATTTTGTGTGATCTCGTCAGGGGGCGGAGCCTATGGAAAAACG 3645
 QY 5591 CCAGCAACCGCGCCTTTTACGTTTCTGCGCCTTTTCTGCGCCTTTTGTCTACATGTTCT 5650
 Db 3646 CCAGCAACCGCGCCTTTTACGTTTCTGCGCCTTTTGTCTACATGTTCT 3705
 QY 5651 TTCTCTGCGTTATCCCTCGATTCTCTGATTAACCGTATTACGCGCTTTGAGTGAGCTGATA 5710
 Db 3706 TTCTCTGCGTTATCCCTCGATTCTCTGATTAACCGTATTACGCGCTTTGAGTGAGCTGATA 3765
 QY 5711 CGCTTCGCGCAGCGCAACGACCGAGCGCAGCGAGTCAGTGACGAGGAGCGGAAGC 5770
 Db 3766 CGCTTCGCGCAGCGCAACGACCGAGCGCAGCGAGTCAGTGACGAGGAGCGGAAGC 3825
 QY 5771 GCCCAATACGAAACCGCCTCTCCCGCGGTTGGCCGATTTCATTAAATGCAG 5822
 Db 3826 GCCCAATACGAAACCGCCTCTCCCGCGGTTGGCCGATTTCATTAAATGCAG 3877

RESULT 14
 US-09-991-209-31
 ; Sequence 31, Application US/09991209
 ; Publication No. US20030024009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dunn-Coleman, Nigel
 ; APPLICANT: Langdon, Timothy
 ; APPLICANT: Morse, Phillip
 ; TITLE OF INVENTION: Manipulation of the Phenolic Acid
 ; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
 ; FILE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
 ; FILE REFERENCE: GC648-2
 ; CURRENT APPLICATION NUMBER: US/09/991,209
 ; CURRENT FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 60/249,608
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 97
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 31
 ; LENGTH: 5337
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: pTUS vector
 US-09-991-209-31

Query Match 47.5%; Score 2768; DB 10; Length 5337;
 Best Local Similarity 96.8%; Pred. No. 0;
 Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY 2835 AGCAGATCGTTCAACAATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTCGCCGTC 2894
 Db 954 AAGCAGATCGTTCAACAATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTCGCCGTC 1013
 QY 2895 TTGCGATGATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTATAATAATTAACATGT 2954
 Db 1014 TTGCGATGATTATCATATAAATTTCTGTTGAATTACGTTAAGCATGTATAATAATTAACATGT 1073
 QY 2955 AATGATGACGTTATTATTAGATGGGTTTTTATGATTAGAGTCCCGCAATTTACATTT 3014
 Db 1074 AATGATGACGTTATTATTAGATGGGTTTTTATGATTAGAGTCCCGCAATTTACATTT 1133
 QY 3015 AATACGATAGAAAAAATAATAGCGCGCAAACTAGGATAAATATATCGCGCGCGTGT 3074
 Db 1134 AATACGATAGAAAAAATAATAGCGCGCAAACTAGGATAAATATATCGCGCGCGTGT 1193
 QY 3075 CATCTATGTTACTAGATCGACTCGAGCATGGGATCCGCGCGCATGCGACGTGCGGC 3134
 Db 1194 CATCTATGTTACTAGATCGATAAAGCTTCTAGAGCGGCGCGTGGAGC-----T 1240
 QY 3135 CCAATTGCCCTATAGTAGGTCGATTAC--AATTCATGGCGCGTGTGTTTACAACGTC 3191
 Db 1241 CCAATTGCCCTATAGTAGGTCGATTACGCGCGCTCACTGGCGCGTGTGTTTACAACGTC 1300

QY	3192	GTGACTGGGAAAACCTGGCGTTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCG	3251	2326	AGTACTCACCAGTCACAGAAAAGCATCTTACGGATGCGATGACAGTAAGAGAAATTATGCA	2385	
Db	1301	GTGACTGGGAAAACCTGGCGTTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCG	1360	QY	4331	GTGCTGCCATAACCATGAGTGATAAACAATCGGGCCAACTTACTTCTGACACGATCGGAG	4390
QY	3252	CCAGCTGCGCGTAATAGCGAAGAGCGCGCACCGANTCGCCCTTCCCAACAGTTGCGCAGCC	3311	Db	2386	GTGCTGCCATAACCATGAGTGATAAACAATCGGGCCAACTTACTTCTGACACGATCGGAG	2445
Db	1361	CCAGCTGCGCGTAATAGCGAAGAGCGCGCACCGANTCGCCCTTCCCAACAGTTGCGCAGCC	1420	QY	4391	GACCGAAGGAGCTAACCGCTTTTTTTCACAACTATGGGGGATCATGTAACTTCGCTTGATC	4450
QY	3312	TGAATGGGGAAT-GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTTA	3370	Db	2446	GACCGAAGGAGCTAACCGCTTTTTTTCACAACTATGGGGGATCATGTAACTTCGCTTGATC	2505
Db	1421	TGAATGGGGAATGGGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTTA	1480	QY	4451	GTGTGGAAACCGGAGCTGAATGAAGCCATACAAACGACGAGCGTGAACACAGATGCTG	4510
QY	3371	CGCGCAGCGTGACCGCTACACTTCCGACGCGCCCTAGCGCCGCTTCCTTTTCCTTC	3430	Db	2506	GTGTGGAAACCGGAGCTGAATGAAGCCATACAAACGACGAGCGTGAACACAGATGCTG	2565
Db	1481	CGCGCAGCGTGACCGCTACACTTCCGACGCGCCCTAGCGCCGCTTCCTTTTCCTTC	1540	QY	4511	TAGCAATGGCAACAAAGTTGGCGCAAACTATTAACTGGGGAATCTTACTCTAGCTTCCC	4570
QY	3431	CTTCTTTCTCGCAACGTTGCGCGCTTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTT	3490	Db	2566	TAGCAATGGCAACAAAGTTGGCGCAAACTATTAACTGGGGAATCTTACTCTAGCTTCCC	2625
Db	1541	CTTCTTTCTCGCAACGTTGCGCGCTTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTT	1600	QY	4571	GGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGACAGGACCACTTCTCGGCTCG	4630
QY	3491	TAGGGTTCGGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGAATTTGGGTGATG	3550	Db	2626	GGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGACAGGACCACTTCTCGGCTCG	2685
Db	1601	TAGGGTTCGGATTTAGTGTCTTTACGGCACCTCGACCGCAAAAACCTTGAATTTGGGTGATG	1660	QY	4631	CCCTTCCGCGCTGGCTTTATTGCTGATAAATCTGGAGCGCGTGGAGCGTGGCTCGCG	4690
QY	3551	GTTCACGTAGTGGGCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCA	3610	Db	2686	CCCTTCCGCGCTGGCTTTATTGCTGATAAATCTGGAGCGCGTGGAGCGTGGCTCGCG	2745
Db	1661	GTTCACGTAGTGGGCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCA	1720	QY	4691	GTATCAATTCGACACCTGGGGCCAGATGCTAAGCCCTCCGCTATCTAGTATCTACACGA	4750
QY	3611	CGTTCTTTAATAGTGGACTCTTGTTCGAACTGGAAACAACTCAACCCCTATCTCGGTCT	3670	Db	2746	GTATCAATTCGACACCTGGGGCCAGATGCTAAGCCCTCCGCTATCTAGTATCTACACGA	2805
Db	1721	CGTTCTTTAATAGTGGACTCTTGTTCGAACTGGAAACAACTCAACCCCTATCTCGGTCT	1780	QY	4751	CGGGAGTCCAGGCAACTATGAGTGAACGAAATAGACAGATCGCTGAGATAGTGCCTCAC	4810
QY	3671	ATTCTTTTGATTTAAGGATTTTCCGATTTTCCGCTATTTGGTTAAAAAATGAGCTGA	3730	Db	2806	CGGGAGTCCAGGCAACTATGAGTGAACGAAATAGACAGATCGCTGAGATAGTGCCTCAC	2865
Db	1781	ATTCTTTTGATTTAAGGATTTTCCGATTTTCCGCTATTTGGTTAAAAAATGAGCTGA	1840	QY	4811	TGATTAAGCAATTTGTAATCTGCAGACCAAGTTTATCTATATATATCTTTAGATGATTTAA	4870
QY	3731	TTTAAACAAATATTTAAACGGAATTTTAAACAAATATTAACGTTTCAAAATTCGCTGATG	3790	Db	2866	TGATTAAGCAATTTGTAATCTGCAGACCAAGTTTATCTATATATATCTTTAGATGATTTAA	2925
Db	1841	TTTAAACAAATATTTAAACGGAATTTTAAACAAATATTAACGTTTCAAAATTCGCTGATG	1891	QY	4871	AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGATATATCTCATGACCA	4930
QY	3791	CGGTATTTTCTCTACGCAATCTGCGGATTTTACAAACGATATTAACGCTTACAAATTT	3850	Db	2926	AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGATATATCTCATGACCA	2985
Db	1892	-----AGGTGGCACTTTTC	1905	QY	4931	AAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCCAGCCCGTAGAAAAAGATCAAA	4990
QY	3851	GGGGAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAATATGATC	3910	Db	2986	AAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCCAGCCCGTAGAAAAAGATCAAA	3045
Db	1906	GGGGAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAATATGATC	1965	QY	4991	GATCTTCTTGAGATCCCTTTTTCGCGCTAACTGCTGCTTGCMAACAAAAAACCCAC	5050
QY	3911	CGCTCATGAGCAATTAACCCCTGATTAATGCTTCAATATTTGAAAAAGGAAGATGA	3970	Db	3046	GATCTTCTTGAGATCCCTTTTTCGCGCTAACTGCTGCTTGCMAACAAAAAACCCAC	3105
Db	1966	CGCTCATGAGCAATTAACCCCTGATTAATGCTTCAATATTTGAAAAAGGAAGATGA	2025	QY	5051	CGCTACAGCGGTGTTTGTTCGCGGATCAAGAGCTACCACTCTTTTTCGAAAGTAA	5110
QY	3971	GTATTCAAATTTCCGTGTCGCCCTTATTCCTTTTTCGCGCATTTTCCCTTCCTGTTT	4030	Db	3106	CGCTACAGCGGTGTTTGTTCGCGGATCAAGAGCTACCACTCTTTTTCGAAAGTAA	3165
Db	2026	GTATTCAAATTTCCGTGTCGCCCTTATTCCTTTTTCGCGCATTTTCCCTTCCTGTTT	2085	QY	5111	CTGCTTTCAGCAGCGCAGATACCAATACTGCTCTCTTAGTGTAGCCGTAGTAGGCC	5170
QY	4031	TTGCTCACCCAGAAACGCTGTGCAAGTAAAGATGCTCAAGATCAGTTGGGTGACCGAG	4090	Db	3166	CTGCTTTCAGCAGCGCAGATACCAATACTGCTCTCTTAGTGTAGCCGTAGTAGGCC	3225
Db	2086	TTGCTCACCCAGAAACGCTGTGCAAGTAAAGATGCTCAAGATCAGTTGGGTGACCGAG	2145	QY	5171	ACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTGCTAACTCTGTTACCAG	5230
QY	4091	TGGGTTACATCGAACTGATCTCAACAGCGGTGAAGATCCTTGAGATTTTTCGCCCGAAG	4150	Db	3226	ACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTGCTAACTCTGTTACCAG	3285
Db	2146	TGGGTTACATCGAACTGATCTCAACAGCGGTGAAGATCCTTGAGATTTTTCGCCCGAAG	2205	QY	5231	TGGCTGTCCAGTGGCGATAGTCTGTTTACCGGGTGGACTCAAGACGATAGTTAC	5290
QY	4151	AACGTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTATCCCGTA	4210	Db	3286	TGGCTGTCCAGTGGCGATAGTCTGTTTACCGGGTGGACTCAAGACGATAGTTAC	3345

Db 3406 GAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCCACGCTTC 3465
Qy 5411 CCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGACAGGTCCGACACGAGAGCGCA 5470
Db 3466 CCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGACAGGTCCGACACGAGAGAGCGCA 3525
Qy 5471 CGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCCCTGTGCGGTTTCGCCAC 5530
Db 3526 CGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCCCTGTGCGGTTTCGCCAC 3585
Qy 5531 TCTGACTGAGCGTGCATTTTGTGATGCTCGTCAGGGGGCGAGCGTATGGAAGAAACG 5590
Db 3586 TCTGACTGAGCGTGCATTTTGTGATGCTCGTCAGGGGGCGAGCGTATGGAAGAAACG 3645
Qy 5591 CCAGCAACGCGGCTTTTACGGTTCCTGGCTTTTGTGCTGCTTTTGTGCTGCTGCTGCT 5650
Db 3646 CCAGCAACGCGGCTTTTACGGTTCCTGGCTTTTGTGCTGCTTTTGTGCTGCTGCTGCT 3705
Qy 5651 TTCTGCGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTGCTGCTGATA 5710
Db 3706 TTCTGCGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTGCTGCTGATA 3765
Qy 5711 CCGCTCCGCGAGCGGACGAGCGAGCGAGTCACTGAGCGAGGAGCGAGCGAGCGAGCG 5770
Db 3766 CCGCTCCGCGAGCGGACGAGCGAGCGAGTCACTGAGCGAGGAGCGAGCGAGCGAGCG 3825
Qy 5771 GCCCAATACCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 5822
Db 3826 GCCCAATACCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 3877

RESULT 15
US-09-991-209-15
; Sequence 15, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5338
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTF10-1 vector
US-09-991-209-15

Query Match 47.5%; Score 2768; DB 10; Length 5338;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCAACACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCGGTC 2894
Db 955 AAGCAGATCGTTCAACACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCGGTC 1014
Qy 2895 TTGCGATGATTATCATATTAATTTCTGTTGAATTAACGTTAAGCATGTAATAAATACATGT 2954
Db 1015 TTGCGATGATTATCATATTAATTTCTGTTGAATTAACGTTAAGCATGTAATAAATACATGT 1074
Qy 2955 AATGATACGTTATTTATGATGGGTTTTATGATAGTCCCGCAATATACATTT 3014
Db 1075 AATGATACGTTATTTATGATGGGTTTTATGATAGTCCCGCAATATACATTT 1134

Qy 3015 AATAGCGATAGAAAAAATAATATAGCGCGCAAACTAGGATAAAATATCGCGCGCGGT 3074
Db 1135 AATAGCGATAGAAAAAATAATATAGCGCGCAAACTAGGATAAAATATCGCGCGCGGT 1194
Qy 3075 CATCTATGTTACTAGATCGACTCGAGCATGCGCGCGCATCGCGCGCATCGCGCGCG 3134
Db 1195 CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGAGC-----T 1241
Qy 3135 CCAATTCGCCCTATAGTGAGTCTGATTAC---AATTCACATGCGCGTGTGTTTACAAAGTC 3191
Db 1242 CCAATTCGCCCTATAGTGAGTCTGATTACGCGCGCTCACTGCGCGTGTGTTTACAAAGTC 1301
Qy 3192 GTGACTGGGAAAAACCTTGGCGTTACCCCACTTAATTCGCTTGCAGCAATCCCCCTTTTCG 3251
Db 1302 GTGACTGGGAAAAACCTTGGCGTTACCCCACTTAATTCGCTTGCAGCAATCCCCCTTTTCG 1361
Qy 3252 CCAGCTGGCGTAATAGGAAAGAGCGCGCGCATTAAGCGCGCGCATTAAGCGCGCGGTGTTA 3311
Db 1362 CCAGCTGGCGTAATAGGAAAGAGCGCGCGCATTAAGCGCGCGCATTAAGCGCGCGGTGTTA 1481
Qy 3312 TGAATGGCGAAT-GGACGCGCCCTGTAGCGCGCGCATTAAGCGCGCGGTGTTA 3370
Db 1422 TGAATGGCGAATGGACGCGCCCTGTAGCGCGCGCATTAAGCGCGCGGTGTTA 1481
Qy 3371 CGCGCAGCGTACCGCTACACTTGCAGCGCGCTAGCGCGCGCTTTCCTTTTCCTTTC 3430
Db 1482 CGCGCAGCGTACCGCTACACTTGCAGCGCGCTAGCGCGCGCTTTCCTTTTCCTTTC 1541
Qy 3431 CTTCCTTTCTCGCCACGTTCCCGCGTTCCTCGCTCAAGCTCTAAATCGGGGCTCCCTT 3490
Db 1542 CTTCCTTTCTCGCCACGTTCCCGCGTTCCTCGCTCAAGCTCTAAATCGGGGCTCCCTT 1601
Qy 3491 TAGGTTTCGATTTAGAGCTTTACGCGACCTCGACCGCAAAACTGATTGTTGGTGTATG 3550
Db 1602 TAGGTTTCGATTTAGTGTCTTACGCGACCTCGACCGCAAAACTGATTGTTGGTGTATG 1661
Qy 3551 GTTCAGTATGCGCATCGCCCTGATAGACGTTTTCGCTTTCGCTTTCGCTTTCGCTTTC 3610
Db 1662 GTTCAGTATGCGCATCGCCCTGATAGACGTTTTCGCTTTCGCTTTCGCTTTCGCTTTC 1721
Qy 3611 CGTTCCTTAAATAGTACGCTTGTTCGCAACGTAAGCAACACTCAACCTTATCGGTCT 3670
Db 1722 CGTTCCTTAAATAGTACGCTTGTTCGCAACGTAAGCAACACTCAACCTTATCGGTCT 1781
Qy 3671 ATTCTTTGATTTAAGGGATTTTCGCGATTTTCGCGCTATTTGTTTAAATAAGTGTGA 3730
Db 1782 ATTCTTTGATTTAAGGGATTTTCGCGATTTTCGCGCTATTTGTTTAAATAAGTGTGA 1841
Qy 3731 TTTAACAATATTTAAGCGAATTTTAAACAATATTAACGTTTAAATTCGCTGATG 3790
Db 1842 TTTAACAATATTTAAGCGAATTTTAAACAATATTAACGTTTAAATTCGCTGATG 1892
Qy 3791 CGGTATTTCTCTTACGCACTGTGCGGTATTTACACCGCATACAGTGGCACTTTTC 3850
Db 1893 -----AGTGGCACTTTTC 1906
Qy 3851 GGGGAAATGTCGCGGAACCCCTATTTGTTTATTTTCTAAATACTCAAAATATGATTC 3910
Db 1907 GGGGAAATGTCGCGGAACCCCTATTTGTTTATTTTCTAAATACTCAAAATATGATTC 1966
Qy 3911 CGCTCATGAGCAATACCCCTGATAAATGCTTCAATAATTTGAAAAAGGAGATGTA 3970
Db 1967 CGCTCATGAGCAATACCCCTGATAAATGCTTCAATAATTTGAAAAAGGAGATGTA 2026
Qy 3971 GTATTCAACATTTCCGTGTCGCCCTTATTCCTTTTTCGCGCATTTTTCCTTCTGTTT 4030
Db 2027 GTATTCAACATTTCCGTGTCGCCCTTATTCCTTTTTCGCGCATTTTTCCTTCTGTTT 2086
Qy 4031 TTGCTCACCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGACCGAG 4090
Db 2087 TTGCTCACCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGACCGAG 2146
Qy 4091 TGGGTTATCATCGAATGGAATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAG 4150

[illegible]

Search completed: June 21, 2004, 21:59:55
Job time : 1571 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 13:47:23 ; Search time 8916 Seconds
(without alignments)
19499.508 Million cell updates/sec

Title: US-09-924-197-1
Perfect score: 5922
Sequence: 1 ctggcagcaggtttccgcg.....tggccgattcattaatgcag 5922

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

EST: *
1:  em_estba: *
2:  em_esthum: *
3:  em_estin: *
4:  em_estnu: *
5:  em_estov: *
6:  em_estpl: *
7:  em_estro: *
8:  em_htc: *
9:  gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_nam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rpd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gsl: *
29: gb_gss2: *

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	1055.8	18.1	1070	9	AJ281552
2	986.4	16.9	1013	12	BM438846
3	924	15.9	1004	9	AJ281480
4	916.2	15.7	973	14	CD458281

5	885.6	15.2	917	14	CD458286	CD458286 Fg08_09a0
6	873	15.0	935	12	BG838279	BG838279 Gc01_10e0
7	865.4	14.9	918	14	CD459092	CD459092 Fg08_08e0
8	841	14.4	841	9	AL042026	AL042026 DKFZp434E
9	832.8	14.3	872	14	CD459085	CD459085 Fg08_08d0
c 10	825	14.2	1073	14	CF289652	CF289652 Fcylcolid8
11	824.6	14.2	854	12	BM438950	BM438950 Iplvr0049
12	819.6	14.1	870	14	CD458333	CD458333 Fg08_09e0
c 13	815.6	14.0	1249	28	BZ572284	BZ572284 msh2_2572
14	814.4	14.0	1126	28	BZ577702	BZ577702 msh2_2572
15	808	13.9	819	14	CD649375	CD649375 msh2_2572
c 16	807.6	13.9	965	28	BZ570738	BZ570738 msh2_2572
17	801.6	13.8	1483	28	BZ575896	BZ575896 msh2_2572
18	797.6	13.7	1011	28	BZ576726	BZ576726 msh2_2572
c 19	785.4	13.5	1574	28	BZ572566	BZ572566 msh2_2572
c 20	777.8	13.4	800	9	AJ281449	AJ281449 4A3A-F4D5
21	777.6	13.4	910	14	CD649387	CD649387 Cvnd0009
22	774.8	13.3	1336	28	BZ575810	BZ575810 msh2_2572
23	774.4	13.3	789	14	CD280920	CD280920 G44224.42
c 24	772.4	13.3	954	9	AL044364	AL044364 DKFZp434C
c 25	771.8	13.3	1067	9	AU081137	AU081137 AU081137
26	770.4	13.2	1370	28	BZ571721	BZ571721 msh2_2025
27	763.2	13.1	780	13	BQ825693	BQ825693 1030129B0
28	757	13.0	759	14	CD279661	CD279661 G43818.35
29	755.4	13.0	1483	28	BZ571475	BZ571475 msh2_1906
30	753.6	12.9	797	12	BM410796	BM410796 EST585123
31	745.4	12.8	786	14	CD458721	CD458721 Fg08_04e0
c 32	745.4	12.8	844	28	BZ574513	BZ574513 msh2_3706
c 33	743.6	12.8	832	12	BG923768	BG923768 602825893
34	741	12.7	741	14	CD279174	CD279174 G44221.83
35	741	12.7	966	28	BZ575002	BZ575002 msh2_4255
c 36	740.4	12.7	1089	9	AU081124	AU081124 AU081124
37	739.8	12.7	1003	28	BZ576686	BZ576686 msh2_5053
38	739.8	12.7	1112	28	BZ577534	BZ577534 msh2_5453
c 39	739.2	12.7	914	28	BZ569398	BZ569398 pac2-164
c 40	738.6	12.7	863	14	CF752100	CF752100 TGD9 Hum
41	733.8	12.6	950	28	BZ571129	BZ571129 msh2_1741
42	733.2	12.6	811	29	ATH517156	AJ517156 Arabidops
43	732.4	12.6	998	28	BZ576702	BZ576702 msh2_5060
44	732.4	12.6	1376	28	BZ571741	BZ571741 msh2_2034
45	730	12.5	730	14	CD281097	CD281097 G44224.38

ALIGNMENTS

RESULT 1	AJ281552/c	1070 bp	mRNA	linear	EST 30-JUN-2000
LOCUS	4A3A-P6F11-F	Anopheles gambiae	immune competent	4A3A	Anopheles
DEFINITION	gambiae cDNA clone 4A3A-P6F11, mRNA sequence.				
ACCESSION	AJ281552				
VERSION	AJ281552.1	GI:6929432			
KEYWORDS	EST.				
SOURCE	Anopheles gambiae (African malaria mosquito)				
ORGANISM	Anopheles gambiae				
REFERENCE	1 (bases 1 to 1070)				
AUTHORS	Donohue, M., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B., and Kafatos, F.C.				
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (12),	6619-6624	(2000)	
MEDLINE	20300950				
PUBMED	10841561				
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerohofstrasse 1, 69117 Heidelberg, Germany.				

```
FEATURES
  source
    Location/Qualifiers
      1..1070
        /organism="Anopheles gambiae"
        /mol_type="mRNA"
        /strain="4A z/r"
        /db_xref="taxon:7165"
        /clone="4A3A-P6F11"
        /cell_line="immune competent 4A3A"
        /lab_host="E. coli DH10B"
        /clone_lib="Anopheles gambiae immune competent 4A3A"
        /note="Vector: p7T3D-Pac (Pharmacia) with a modified
        polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
        forward priming site which reads from the 3' end of the
        cDNA. The 4A3A is a directionally cloned and normalized
        cDNA library that was constructed from the 4A3A cell line
        cDNA library primed cDNA according to: Bonaldo, Lennon & Soares
        (1996): Normalization and Subtraction: Two approaches To
        Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN
  Query Match      18.1%; Score 1055.8; DB 9; Length 1070;
  Best Local Similarity 99.7%; Pred. No. 2.1e-256; Indels 1; Gaps 1;
  Matches 1068; Conservative 0; Mismatches 2;

QY 4527 GTTGGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCGGCAACAATTAATAGA 4586
DB 1070 GTTGGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCGGCAACAATTAATAGA 1011
QY 4587 CTGGATGGAGGGGATAAAGTTGCGAGCACCTTCTGCGCTCGGCCCTTCCGGCTGGCTG 4646
DB 1010 CTGGATGGAGGGGATAAAGTTGCGAGCACCTTCTGCGCTCGG-CTTCCGGCTGGCTG 952
QY 4647 GTTTATTGCTGATAAATCTGGAGCCGCTGAGCGTGGCTCGCGGTATCATTTGCAGCACT 4706
DB 951 GTTTATTGCTGATAAATCTGGAGCCGCTGAGCGTGGCTCTCGCGGTATCATTTGCAGCACT 892
QY 4707 GGGCCAGATGTTAAAGCCCTCCCGTATCGTAGTTATCTACAGCGGGAGTCAGCAAC 4766
DB 891 GGGCCAGATGTTAAAGCCCTCCCGTATCGTAGTTATCTACAGCGGGAGTCAGCAAC 832
QY 4767 TATGGATGAACGAAATAGACAGATCGCTGAGATAGTGTCTCTGATTAAGCATTTGGTA 4826
DB 831 TATGGATGACGAAATAGACAGATCGCTGAGATAGTGTCTCTGATTAAGCATTTGGTA 772
QY 4827 ACTGTGACACCAAGTTTACTCATATATCTTGTAGTTGATTTAAACTTCAATTTAAAT 4886
DB 771 ACTGTGACACCAAGTTTACTCATATATCTTGTAGTTGATTTAAACTTCAATTTAAAT 712
QY 4887 TAAAGGATCTAGTGAAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAAAGTGA 4946
DB 711 TAAAGGATCTAGTGAAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAAAGTGA 652
QY 4947 GTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGGATCTTTTGAGATCC 5006
DB 651 GTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGGATCTTTTGAGATCC 592
QY 5007 TTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGGATCTTTTGAGATCC 5066
DB 591 TTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGGATCTTTTGAGATCC 532
QY 5067 TTGTTTCGCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACTGGCTTCAGCAGC 5126
DB 531 TTGTTTCGCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACTGGCTTCAGCAGC 472
QY 5127 GCAGATACCAAAATCTGTCCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGACTC 5186
DB 471 GCAGATACCAAAATCTGTCCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGACTC 412
QY 5187 TGTAGCACCGCTACATACCTCGCTCTGCTTAATCTGTTACAGTGGCTGCTGCAGTGG 5246
DB 411 TGTAGCACCGCTACATACCTCGCTCTGCTTAATCTGTTACAGTGGCTGCTGCAGTGG 352
QY 5247 CGATAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAGGCGCAGCG 5306
```

```

|||||
351 CGATAAGTCTGTCTTACCGGTTGGACTCAAGCAGTAGTTACCGGATAGGCGCAGCG 292
|||||
5307 GTCCGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAAGCAGCTACACGA 5366
|||||
291 GTCCGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAAGCAGCTACACGA 232
|||||
5367 ACTGAGATACCTACAGCGTGTAGTATGAGAAAGCGCCAGCTTCCCGAAGGAGAAAGCG 5426
|||||
231 ACTGAGATACCTACAGCGTGTAGTATGAGAAAGCGCCAGCTTCCCGAAGGAGAAAGCG 172
|||||
5427 GCAGAGTATCGGTAAAGCGGCGAGGTCGAAACAGGAGAGCGCAGAGGAGCTTCCAGG 5486
|||||
171 GCAGAGTATCGGTAAAGCGGCGAGGTCGAAACAGGAGAGCGCAGAGGAGCTTCCAGG 112
|||||
5487 GGGAAACCGCTGGTATCTTTATAGTCTCTGTCGGTTTCGCCACCTCTGACTTGAGGCTG 5546
|||||
111 GGGAAACCGCTGGTATCTTTATAGTCTCTGTCGGTTTCGCCACCTCTGACTTGAGGCTG 52
|||||
5547 ATTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAACAGCCAGCAA 5597
|||||
51 ATTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAACAGCCAGCAA 1

RESULT 2
BM438846 1013 bp mRNA linear EST 31-JAN-2002
LOCUS IplvR00157 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
DEFINITION sequence.
ACCESSION BM438846
VERSION BM438846.1 GI:18460568
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 1013)
Feng, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.
Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
Unpublished (2002)
Contact: Liu Zi
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
  1..1013
    /organism="Ictalurus punctatus"
    /mol_type="mRNA"
    /db_xref="taxon:7998"
    /clone_lib="Liver cDNA library"
    /note="Organ: Liver; Vector: pSport1; Site_1: NotI;
    Site_2: SalI"

FEATURES
  source
    Query Match      16.9%; Score 986.4; DB 12; Length 1013;
    Best Local Similarity 99.5%; Pred. No. 8.6e-239;
    Matches 1009; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 4012 GCATTTTGCCTCTCTGTTTGTCTCACCAGAACGCTGGTGAAGTAAAGATGCTGAA 4071
DB 1 GCATTTTGCCTCTCTGTTTGTCTCACCAGAACGCTGGTGAAGTAAAGATGCTGAA 60
|||||
4072 GATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAGTCCTT 4131
DB 61 GATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAGTCCTT 120
```



```

QY 4132 GAGAGTTTTCGCCCGAAGAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 4191
Db 121 GAGAGTTTTCGCCCGAAGAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 180
QY 4192 GCGCGGTATTATCCGTTATTGACCGCGGGAAGAGCACTCGTTCGCGGCAATACACTAT 4251
Db 181 GCGCGGTATTATCCGTTATTGACCGCGGGAAGAGCACTCGTTCGCGGCAATACACTAT 240
QY 4252 TCTCAGAAATGACTTGGTTGAGTACTCACAGTACAGAAAGAGCACTTTTACGATGGCATG 4311
Db 241 TCTCAGAAATGACTTGGTTGAGTACTCACAGTACAGAAAGAGCACTTTTACGATGGCATG 300
QY 4312 ACAGTAGAGAAATATGAGTGTCTGCCAATACCAATGAGTGTATACACTGCGGCAACTTA 4371
Db 301 ACAGTAGAGAAATATGAGTGTCTGCCAATACCAATGAGTGTATACACTGCGGCAACTTA 360
QY 4372 CTTCTGCAACGATCGGAGGACCGAAGAGTACACCGCTTTTTCGCAAAATGCGGGAT 4431
Db 361 CTTCTGCAACGATCGGAGGACCGAAGAGTACACCGCTTTTTCGCAAAATGCGGGAT 419
QY 4432 C-ATGTAACCTCGCTTGCATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGA 4490
Db 420 CAATGTAACCTCGCTTGCATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGA 479
QY 4491 GCGTGACACCAAGATGCTGTAGCAATGGCAACACGTTGCGCAAACTATTAACTGGCGA 4550
Db 480 GCGTGACACCAAGATGCTGTAGCAATGGCAACACGTTGCGCAAACTATTAACTGGCGA 539
QY 4551 ACTACTTACTCTAGTCTCCGCGCAACATTAATAGACTGATGAGCGGATAAAGTTGC 4610
Db 540 ACTACTTACTCTAGTCTCCGCGCAACATTAATAGACTGATGAGCGGATAAAGTTGC 599
QY 4611 AGGACCACTTCTCGGCTCGGCCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGGAGC 4670
Db 600 AGGACCACTTCTCGGCTCGGCCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGGAGC 659
QY 4671 CGGTGAGCGTGGTCTCGCGGTATCATTTGACGACCTGGGCGCAGATGGTAAGCCCTCCCG 4730
Db 660 CGGTGAGCGTGGTCTCGCGGTATCATTTGACGACCTGGGCGCAGATGGTAAGCCCTCCCG 719
QY 4731 TATCGTAGTATCTACACGACGGGAGTACGGCAACTATGGATGAACGAAATAGACAGAT 4790
Db 720 TATCGTAGTATCTACACGACGGGAGTACGGCAACTATGGATGAACGAAATAGACAGAT 779
QY 4791 CGCTGAGATAGGTGCTCTACTGATTAAGCACTGTAACGTCAGACCAAGTTTACTCATA 4850
Db 780 CGCTGAGATAGGTGCTCTACTGATTAAGCACTGTAACGTCAGACCAAGTTTACTCATA 839
QY 4851 TATACTTTAGATTGATTTAAATCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCT 4910
Db 840 TATACTTTAGATTGATTTAAATCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCT 899
QY 4911 TTTTGATATCTCATGACCAAAATCCCTTAAAGTGTGTTTCGTCACCTGAGCGTCAGA 4970
Db 900 TTTTGATATCTCATGACCAAAATCCCTTAAAGTGTGTTTCGTCACCTGAGCGTCAGA 959
QY 4971 CCCGTAGAAAAGATCAAGAGTCTTCTGAGATCCTTTTTCGCGGTAAT 5024
Db 960 CCCGTAGAAAAGATCAAGAGTCTTCTGAGATCCTTTTTCGCGGTAAT 1013

```

```

RESULT 3
AJ281480/c
LOCUS
DEFINITION
4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P4G8, mRNA sequence.
ACCESSION
AJ281480
VERSION
AJ281480.1 GI:6929360
KEYWORDS
EST.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

```

REFERENCE
AUTHORS
Dimopoulos G., Kasavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
and Kafatos, F.C.
TITLE
Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE
20300950
PUBMED
10841561
COMMENT
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerohofstrasse 1, 69117 Heidelberg, Germany.
FEATURES
Location/Qualifiers
1..1004
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4G8"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches to
Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN
Query Match 15.9%; Score 924; DB 9; Length 1004;
Best Local Similarity 99.0%; Pred. No. 5.9e-223;
Matches 1001; Conservative 1; Mismatches 2; Indels 7; Gaps 7;

```

```

QY 4616 CACTTCTCGCTCGGCCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGGAGCGCGTG 4675
Db 1004 CACTTCTCGCTCGGCCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGGAGCGCGTG 948
QY 4676 AGCGTGGGTCTCGCGGTATCATTTGACGACCTGGGCGCAGATGTAAGCCCTCCGATCG 4735
Db 947 AGCGT-GGTCTCGCGGTATCATTTGACGACCT-GGGCCARATGGTAAGCCCTCCGATCG 890
QY 4736 TAGTTATCTACAGCGGGAGTCTAGGCAACTATGGATGAACGAAATAGACAGATCGCTG 4795
Db 889 TAG-TATCTACAGCGGGAGTCTAGGCAACTATGGATGAACGAAATAGACAGATCGCTG 831
QY 4796 AGATAGGTGCTCTACTGATTAAGCACTGTAACCTCTGACACCAAGTTTACTCATATATAC 4855
Db 830 AGATA-GTGCCCTCTACTGATTAAGCACTGTAACCTCTGACACCAAGTTTACTCATATATAC 772
QY 4856 TTTAGATTGATTTAAATCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTTCG 4915
Db 771 TTTAGATTGATTTAAATCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTTCG 712
QY 4916 ATAATCTCATGACCAAAATCCCTTAAAGTGTGTTTCGTTCCACTGAGCGTCAGACCCCG 4975
Db 711 ATAATCTCATGACCAAAATCCCTTAAAGTGTGTTTCGTTCCACTGAGCGTCAGACCCCG 652
QY 4976 TAGAAAAGATCAAGAGTCTTCTGAGATCCTTTTTCGCGGTAATCTGCTGCTTCG 5035
Db 651 TAGAAAAGATCAAGAGTCTTCTGAGATCCTTTTTCGCGGTAATCTGCTGCTTCG 592
QY 5036 AAACAAAAAACCCCGCTACCGCGGTGTTTTCGCGGATCAAGAGTACCACTC 5095
Db 591 AAACAAAAAACCCCGCTACCGCGGTGTTTTCGCGGATCAAGAGTACCACTC 532
QY 5096 TTTTTCGAAAGTAACTGGGCTTCAGAGCGCGCATACCAAACTCTCTCTCTAGTGT 5155

```

```

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
1 (bases 1 to 1004)
Dimopoulos, G., Kasavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
10841561
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerohofstrasse 1, 69117 Heidelberg, Germany.
Location/Qualifiers
1..1004
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4G8"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches to
Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN
Query Match 15.9%; Score 924; DB 9; Length 1004;
Best Local Similarity 99.0%; Pred. No. 5.9e-223;
Matches 1001; Conservative 1; Mismatches 2; Indels 7; Gaps 7;

```



```

Db      923  TCGTAGTATCTACAGSAGGGAGTCAGCAACTGATGATGACGAATAGA 973
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 5
CD458286          917 bp  mRNA  linear  EST 03-JUN-2003
LOCUS             FG08_09a03_R Fg08 AAFRC ECORC Fusarium graminearum complex_substrate
DEFINITION        Gibberella zeae cDNA clone Fg08_09a03, mRNA sequence.
ACCESSION         CD458286
VERSION           CD458286.1 GI:31373026
KEYWORDS          EST.
SOURCE            Gibberella zeae
ORGANISM          Gibberella zeae
REFERENCE         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS           Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
                  Watson, R.J., Heyls, R., Chapados, J., Couroux, P., Harris, L.J.,
                  Hattori, J., Iacox, C., Ouellet, T., Robert, L.S., Singh, J.A.,
                  Sprott, D., and Tinker, N.A.
TITLE             A cDNA library prepared from Fusarium graminearum grown on a
                  complex plant substrate
JOURNAL           Unpublished (2003)
COMMENT           Contact: Watson, Robert.J.
                  Eastern Cereal and Oilseed Research Centre
                  Agriculture and Agri-food Canada
                  Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
                  CANADA
                  Tel: (613) 759-1655
                  Fax: (613) 759-1701
                  Email: watsonrj@agr.gc.ca.
FEATURES          Location/Qualifiers
source            1..917
                  /organism="Gibberella zeae"
                  /mol_type="mRNA"
                  /strain="DAOM 180378"
                  /db_xref="taxon:5518"
                  /clone="Fg08_09a03"
                  /tissue_type="Mycelium"
                  /dev_stage="Asexual"
                  /lab_host="E. coli DH10B"
                  /clone_lib="Fg08 AAFRC ECORC Fusarium graminearum_complex_s
                  ubstrate"
                  /note="Vector: pBluescript II+; Site 1: EORI; Site 2:
                  XhoI; Fusarium graminearum grown on a complex plant
                  substrate-- wheat leaves treated to remove most of the low
                  molecular weight, water-soluble components."
ORIGIN
Query Match      15.2%; Score 885.6; DB 14; Length 917;
Best Local Similarity 99.6%; Pred. No. 3.2e-213;
Matches 888; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3833 ATACAGTGGCGACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTCTAAA 3892
Db      26  ATTAGTGGCGACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTCTAAA 85
QY 3893 TACATTCAAATATGATCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATAT 3952
Db      86  TACATTCAAATATGATCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATAT 145
QY 3953 GAAAAGGAAGATGATGATATCAACATTTCCGTGTCGCCCTTATTCCTTTTGGG 4012
Db      146 GAAAAGGAAGATGATGATATCAACATTTCCGTGTCGCCCTTATTCCTTTTGGG 205
QY 4013 CATTTTGCTTCTCTTTTGTCTACCCAGAACGCTGGTGAAGATAAGATGCTGAAG 4072
Db      206 CATTTTGCTTCTCTTTTGTCTACCCAGAACGCTGGTGAAGATAAGATGCTGAAG 265
QY 4073 ATCAGTTGGGTGCACAGATGGGTTCATCGACTGATCTCAACAGCGTAAGATCCTTG 4132
Db      266 ATCAGTTGGGTGCACAGATGGGTTCATCGACTGATCTCAACAGCGTAAGATCCTTG 325

```

```

QY 4133 AGAGTTTTCGCCCCGAGAACGTTTTCOAATGATGAGCACTTTTAAAGTTCTGCTATG 4192
Db      326 AGAGTTTTCGCCCCGAGAACGTTTTCOAATGATGAGCACTTTTAAAGTTCTGCTATG 385
QY 4193 GCGCGGTATTATCCCGTATTGACGCGGGCGAGACAACTCGGTGCGCGCATACACTATT 4252
Db      386 GCGCGGTATTATCCCGTATTGACGCGGGCGAGACAACTCGGTGCGCGCATACACTATT 445
QY 4253 CTCAGAATGACTTGGTTGAGTACTCACAGTTCACAGAAAGCATCTTACGGATGCAACA 4312
Db      446 CTCAGAATGACTTGGTTGAGTACTCACAGTTCACAGAAAGCATCTTACGGATGCAACA 505
QY 4313 CAGTAAGAGATTTATGAGTGTGCTGCTCAATAACATGAGTGATAACACTCGGCGCAACTTAC 4372
Db      506 CAGTAAGAGATTTATGAGTGTGCTGCTCAATAACATGAGTGATAACACTCGGCGCAACTTAC 565
QY 4373 TTCTGACAAACGATCGGAGGACCGAAGGAGCTAAACGCTTTTTCGACAAACATGGGGGATC 4432
Db      566 TTCTGACAAACGATCGGAGGACCGAAGGAGCTAAACGCTTTTTCGACAAACATGGGGGATC 625
QY 4433 ATGTAACCTCGCTTGTGATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGC 4492
Db      626 ATGTAACCTCGCTTGTGATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGC 685
QY 4493 GTGACACACGATGCTGTGAGCAATGCGCAACAAACGTTGCGCAAACTATTAACTGGCGAAC 4552
Db      686 GTGACACACGATGCTGTGAGCAATGCGCAACAAACGTTGCGCAAACTATTAACTGGCGAAC 745
QY 4553 TACTTACTCTAGCTTCCCGGCGCAACAAATTAAGACTGAGTGGAGCGGATGAATGTCAG 4612
Db      746 TACTTACTCTAGCTTCCCGGCGCAACAAATTAAGACTGAGTGGAGCGGATGAATGTCAG 805
QY 4613 GACCACCTTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATAAATCTGGAGCCG 4672
Db      806 GACCACCTTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATAAATCTGGAGCCG 865
QY 4673 GTGAGCGTGGGTCTCGCGGTATCATTTGACGACTGGGCGCGAGATGTTAAGCC 4724
Db      866 GTGAGCGTGGGTCTCGCGGTATCATTTGACGACTGGGCGCGAGATGTTAAGCC 917

```

```

RESULT 6
BG838279
LOCUS             BG838279
DEFINITION        Gc01_10e07_R Gc01 AAFRC ECORC cold stressed Glycine clandestina
                  Glycine clandestina cDNA clone Gc01_10e07, mRNA sequence.
ACCESSION         BG838279
VERSION           BG838279.1 GI:14204601
KEYWORDS          EST.
SOURCE            Glycine clandestina
ORGANISM          Glycine clandestina
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                  rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                  Glycine.
REFERENCE         1. (bases 1 to 935)
AUTHORS           Singh, J.A., Farah, S., Chapados, J., Couroux, P., De Moors, A.,
                  Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and
                  Tinker, N.A.
TITLE             Expressed Sequence Tags from Cold-Stressed Glycine clandestina
JOURNAL           Unpublished (2001)
COMMENT           Contact: Singh, J.A.
                  Eastern Cereal and Oilseed Research Centre
                  Agriculture and Agri-food Canada
                  KM Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
                  0C6, Canada
                  Tel: (613) 759-1662
                  Fax: (613) 759-1701
                  Email: singhja@em.agr.ca.
FEATURES          Location/Qualifiers
source            1..935
                  /organism="Glycine clandestina"

```

Db 812 GGACCATTCTGGCTCGGCTTCGGCTGGTGGKTTATTGCTGATAWATCTGGRGCC 871

Qy 4672 GGTGAGCGTGGTCTCGCGGTATCATTCGAGCATCGGGCGAGATGTAAGCCCTCC 4728

Db 872 GKGAGCGTGGKCTCGCGGTATCATTCGAGCMCTGGGGCGAGATGTAAGCCCTCC 928

RESULT 7

CD459092 918 bp mRNA linear EST 03-JUN-2003

LOCUS Fg08_08e02 R Fg08_AAFc_ECORC_Fusarium_graminearum_complex_substrate

DEFINITION Gibberella_zeae cDNA clone Fg08_08e02, mRNA sequence.

ACCESSION CD459092

VERSION CD459092.1 GI:31373832

KEYWORDS EST.

SOURCE Gibberella zeae

ORGANISM Gibberella zeae

REFERENCE Watson, R.J., Heyes, R., Chapados, J., Couroux, P., Harris, L.J., Hattori, J., Lacroix, C., Ouellet, T., Robert, L.S., Singh, J.A., Spott, D. and Tinker, N.A.

AUTHORS A cDNA library prepared from Fusarium graminearum grown on a complex plant substrate

TITLE Unpublished (2003)

JOURNAL Contact: Watson, Robert.J.

COMMENT Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA

Tel: (613) 759-1655

Fax: (613) 759-1701

Email: watsonrj@agr.gc.ca.

FEATURES

1..918

Location/Qualifiers

/organism="Gibberella zeae"

/mol_type="mRNA"

/strain="DAOM 180378"

/db_xref="taxon:5518"

/clone="Fg08_08e02"

/tissue_type="Mycelium"

/dev_stage="Asexual"

/lab_host="E. coli DH10B"

/clone_lib="Fg08_AAFc_ECORC_Fusarium_graminearum_complex_substrate"

/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2: XhoI; Fusarium graminearum grown on a complex plant substrate-- wheat leaves treated to remove most of the low molecular weight, water-soluble components."

ORIGIN

Query Match 14.9%; Score 865.4; DB 14; Length 918;

Best Local Similarity 99.2%; Pred. No. 4.4e-208;

Matches 888; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

Qy 3833 ATACAGTGGCATTTCGGGGAAATGTCGGCGAACCCTATTGTTTCTTAA 3892

Db 24 ATTAGTGGCATTTCGGGGAAATGTCGGCGAACCCTATTGTTTCTTAA 83

Qy 3893 TACATTCAAATATGATTCGGCTCATGAGACAATAACCTGATAAATGCTCAATAATTT 3952

Db 84 TACATTCAAATATGATTCGGCTCATGAGACAATAACCTGATAAATGCTCAATAATTT 143

Qy 3953 GAAAAGGAAGAGATGAGTATTCACATTCCTGTCGCCCTTATTCCTTTTGGG 4012

Db 144 GAAAAGGAAGAGATGAGTATTCACATTCCTGTCGCCCTTATTCCTTTTGGG 203

Qy 4013 CATTTGCTTCTGTTTTCCTGCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAG 4072

Db 204 CATTTGCTTCTGTTTTCCTGCTCACCAGAGACGCTGGTGAAGTAAAGATGCTGAAG 263

Qy 4073 ATCAGTTGGTGCAGGTGGTTTACATCGAATGATCTCAACAGCGGTGAATCTCTTG 4132

/mol_type="mRNA"

/cultivar="1035"

/db_xref="taxon:45687"

/clone="Gc01_10e07"

/tissue_type="Leaves, stem"

/clone_lib="Gc01_AAFc_ECORC_cold_stressed_Glycine_clandestina"

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-3 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pBluescript."

ORIGIN

Query Match 15.0%; Score 873; DB 12; Length 935;

Best Local Similarity 97.9%; Pred. No. 5.1e-210;

Matches 878; Conservative 14; Mismatches 4; Indels 1; Gaps 1;

Qy 3833 ATACAGTGGCATTTCGGGAAATGTCGGCGAACCCTATTGTTTCTTAA 3892

Db 32 ATTAGTGGCATTTCGGGAAATGTCGGCGAACCCTATTGTTTCTTAA 91

Qy 3893 TACATTCAAATATGATTCGGCTCATGAGACAATAACCTGATAAATGCTCAATAATTT 3952

Db 92 TACATTCAAATATGATTCGGCTCATGAGACAATAACCTGATAAATGCTCAATAATTT 151

Qy 3953 GAAAAGGAAGAGATGAGTATTCACATTCCTGTCGCCCTTATTCCTTTTGGG 4012

Db 152 GAAAAGGAAGAGATGAGTATTCACATTCCTGTCGCCCTTATTCCTTTTGGG 211

Qy 4013 CATTTGCTTCTGTTTTCCTGCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAG 4072

Db 212 CATTTGCTTCTGTTTTCCTGCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAG 271

Qy 4073 ATCAGTTGGTGCAGGTGGTTTACATCGAATGATCTCAACAGCGGTGAATCTCTTG 4132

Db 272 ATCAGTTGGTGCAGGTGGTATTCGAATGATCTCAACAGCGGTGAATCTCTTG 331

Qy 4133 AGAGTTTTCGCCCCGGAAGACGTTTTCGAATGATGACACTTTTAAAGTTCGCTATG 4192

Db 332 AGAGTTTTCGCCCCGGAAGACGTTTTCGAATGATGACACTTTTAAAGTTCGCTATG 391

Qy 4193 GCGCGTATTTATCCGTTATTCAGCGCGGCAAGCAACTCGTTCGCCGATACACTATT 4252

Db 392 GCGCGTATTTATCCGTTATTCAGCGCGGCAAGCAACTCGTTCGCCGATACACTATT 451

Qy 4253 CTGAGATGACTTGGTTGAGTACTCTACAGTCTCAGAAAAGCATCTTACGGATGGCATGA 4312

Db 452 CTGAGATGACTTGGTTGAGTACTCTACAGTCTCAGAAAAGCATCTTACGGATGGCATGA 511

Qy 4313 CAGTAAGAGAAATATGAGTCTGCCATAACATGATGATAACACTGCGG-CCAACTTA 4371

Db 512 CAGTAAGAGAAATATGAGTCTGCCATAACATGATGATAACACTGCGGCGCCAACTTA 571

Qy 4372 CTTCTGACACGATTCGAGACGCAAGAGACTACCGCTTTTTCGCAACATGGGGAT 4431

Db 572 CTTCTGACACGATTCGAGACGCAAGAGACTACCGCTTTTTCGCAACATGGGGAT 631

Qy 4432 CATGTAATCGCTTGTATGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGAG 4491

Db 632 CATGTAATCGCTTGTATGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGAG 691

Qy 4492 CGTGACACGATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4551

Db 692 CGTGACACGATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751

Qy 4552 CTACTTACTCTAGCTTCCCGCAACAATTAATAGATGATGATGATGATGATGATGATGATGAT 4611

Db 752 CTACTTACTCTAGCTTCCCGCAACAATTAATAGATGATGATGATGATGATGATGATGATGAT 811

Qy 4612 GGACCACTTCTGCGCTCGGCCCTTCGGCTGGTGTATTCGCTGATTAATCTGAGGCC 4671

```

Db 264 ATCAGTTCGGTGCAGAGTGGGTACATCGAATCGATCTCAACAGCGTAAATCCTTG 323
QY 4133 AGAGTTTTTCGCCCGCAAGAACCTTTTCCAAATGATGAGCACATTTTAAAGTTCGTATGTG 4192
Db 324 AGAGTTTTTCGCCCGCAAGAACCTTTTCCAAATGATGAGCACATTTTAAAGTTCGTATGTG 383
QY 4193 GCGGGTATATCCGCTATTGACGCGCGGGCAAGAGCAACTCGGTCCGCGCATACACTATT 4252
Db 384 GCGGGTATATCCGCTATTGACGCGCGGGCAAGAGCAACTCGGTCCGCGCATACACTATT 443
QY 4253 CTCAGATGACTTGGTTGAGTACTCACAGTCACAGAAAGCATCTTACGGATGGCATGA 4312
Db 444 CTCAGATGACTTGGTTGAGTACTCACAGTCACAGAAAGCATCTTACGGATGGCATGA 503
QY 4313 CAGTAAGAGAAATTATGAGTCTGCTGCAATACCA-TGAGTGAATACACTGCGGCGCAACTTA 4371
Db 504 CAGTAAGAGAAATTATGAGTCTGCTGCAATACCA-TGAGTGAATACACTGCGGCGCAACTTA 563
QY 4372 CTTCTGACACGATCGGAGGACCGAAGAGCTAACCGCTTTTTCACAAACATGGGGAT 4431
Db 564 CTTCTGACACGATCGGAGGACCGAAGAGCTAACCGCTTTTTCACAAACATGGGGAT 623
QY 4432 CATGTAATCGCTTGTATGTTGGAAACCGGAGCTGAATGAAGCCATACCAAAACGAGAG 4491
Db 624 CATGTAATCGCTTGTATGTTGGAAACCGGAGCTGAATGAAGCCATACCAAAACGAGAG 683
QY 4492 CGTGACACACGATCGCTGAGCAATGCGACACACCTGTCGCAACACTTAACTTCGGGAA 743
Db 684 CGTGACACACGATCGCTGAGCAATGCGACACACCTGTCGCAACACTTAACTTCGGGAA 743
QY 4552 CTACTTACTCTAGCTTCCCGGCAACAAATTAAGTACCTGGATGGAGCGGATAAGTTGCA 4611
Db 744 CTACTTACTCTAGCTTCCCGGCAACAAATTAAGTACCTGGATGGAGCGGATAAGTTGCA 803
QY 4612 GGAACCACTTCGCGCTCGGCCCTTCGCGTGGCTGTTTATGCTGATAAATCTGGAGCC 4671
Db 804 GGAACCACTTCGCGCTCGGCCCTTCGCGTGGCTGTTTATGCTGATAAATCTGGAGCC 863
QY 4672 GGTGAGCGTGGGTCTGCGGT-ATCATTGACGACTGGGCGGAGATGGTAAGGCC 4725
Db 864 GGTGAGCGTGGGTCTGCGGTAACTATTGACGCMCTGGGCGGAGATGGTAAGGCC 918

RESULT 8
LOCUS DKFZp434E111_r1 434 (synonym: hres3) Homo sapiens linear EST 04-SEP-2003
DEFINITION DKFZp434E111_5', mRNA sequence.
ACCESSION AL042026
VERSION AL042026.1 GI:5421372
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 841)
Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Poustka, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp434E111) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

```

FEATURES

source

Location/Qualifiers

1..841

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp434E111"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="434 (synonym: hres3)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

```

Query Match      14.4%; Score 841; DB 9; Length 841;
Best Local Similarity 100.0%; Pred. No. 6.7e-202;
Matches 841; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3873 TATTTGTTATTTTCTAAATACATTTCAAAATATGATATCCGCTCATGAGACAATAACCCCTG 3932
Db 1 TATTTGTTATTTTCTAAATACATTTCAAAATATGATATCCGCTCATGAGACAATAACCCCTG 60
QY 3933 ATAAATGCTTCAATAATATTGAAAAGCAAGATATGAGTATTTCAACATTTCCGTTGCGC 3992
Db 61 ATAAATGCTTCAATAATATTGAAAAGCAAGATATGAGTATTTCAACATTTCCGTTGCGC 120
QY 3993 CTTTATTCCTTTTTCGGGCATTTTGCCTTTCCTGTTTTCCTGTTTTCCTGTTTTCCTGTTT 4052
Db 121 CTTTATTCCTTTTTCGGGCATTTTGCCTTTCCTGTTTTCCTGTTTTCCTGTTTTCCTGTTT 180
QY 4053 GAAAGTAAAGATGCTGAAATCAGTTGGTGTGACGAGTGGGTTCATCGAATCGGATCT 4112
Db 181 GAAAGTAAAGATGCTGAAATCAGTTGGTGTGACGAGTGGGTTCATCGAATCGGATCT 240
QY 4113 CAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTTCATATGATGAGCAC 4172
Db 241 CAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTTCATATGATGAGCAC 300
QY 4173 TTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATTGACGCGGGCAAGAGCAACT 4232
Db 301 TTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATTGACGCGGGCAAGAGCAACT 360
QY 4233 CGTCCGCGGATACATCTTCTCAGAAATGACTTTGGTTGAGTACTCTACCACTCAGAGAAA 4292
Db 361 CGTCCGCGGATACATCTTCTCAGAAATGACTTTGGTTGAGTACTCTACCACTCAGAGAAA 420
QY 4293 GCATCTTACCGATGGCATGACAGTAAGAGAAATTTATCGAGTGTGCTGCCATTAACATGATGA 4352
Db 421 GCATCTTACCGATGGCATGACAGTAAGAGAAATTTATCGAGTGTGCTGCCATTAACATGATGA 480
QY 4353 TAACTCTGCGGCAACTTACTTCTGACAAACGATCGGAGGACCGAGAGGAGCTAACCCCTTT 4412
Db 481 TAACTCTGCGGCAACTTACTTCTGACAAACGATCGGAGGACCGAGAGGAGCTAACCCCTTT 540
QY 4413 TTTGCAACATGCGGGATCATGTAATCGCTTGTATCGTTGGGAACCGGAGCTGAATGA 4472
Db 541 TTTGCAACATGCGGGATCATGTAATCGCTTGTATCGTTGGGAACCGGAGCTGAATGA 600
QY 4473 AGCCATACCAACACGAGCGTGACACCAAGTCTGCTAGCAATGGCAACAGCTTGGC 4532
Db 601 AGCCATACCAACACGAGCGTGACACCAAGTCTGCTAGCAATGGCAACAGCTTGGC 660
QY 4533 CAACTATTAACTGCGGAACACTTACTTACTGCTTCCCGGCAACAAATTAATAGACTGGAT 4592
Db 661 CAACTATTAACTGCGGAACACTTACTTACTGCTTCCCGGCAACAAATTAATAGACTGGAT 720
QY 4593 GGAGCGGATAAAGTTGAGGACCACTTCTCGCTTCGCCCTTCGCGTGGCTGGCTGTTAT 4652
Db 721 GGAGCGGATAAAGTTGAGGACCACTTCTCGCTTCGCCCTTCGCGTGGCTGGCTGTTAT 780
QY 4653 TGCTGATAAACTCGAGCGCGTGAGCGGTGCTCGCGGTATCATTTGAGCACTGGGGCC 4712
Db 781 TGCTGATAAACTCGAGCGCGTGAGCGGTGCTCGCGGTATCATTTGAGCACTGGGGCC 840

```

Tue Jun 22 14:25:52 2004

```

QY      4713 A 4713
Db      841 A 841

RESULT 9
CD459085      872 bp mRNA linear EST 03-JUN-2003
LOCUS      Fg08_08d03_R Fg08_AAF_C_ECORC_Fusarium_graminearum_complex_substrate
DEFINITION  Gibberella zeae cDNA clone Fg08_08d03, mRNA sequence.
ACCESSION  CD459085
VERSION    CD459085.1 GI:31373825
SOURCE     Gibberella zeae
ORGANISM   Gibberella zeae
REFERENCE  1 (bases 1 to 872)
AUTHORS   Watson, R.J., Heyes, R., Chapados, J., Couroux, P., Harris, L.J.,
Hattori, J., Iacoiu, C., Ouellet, T., Robert, L.S., Singh, J.A.,
Sprott, D. and Tinker, N.A.
TITLE     A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
JOURNAL   Unpublished (2003)
COMMENT   Contact: Watson, Robert J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.

FEATURES
Source
1..872
Location/Qualifiers
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_08d03"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAF_C_ECORC_Fusarium_graminearum_complex_s
ubstrate"
/note="Vector: pBluescript II+; Site_1: EcoRI; Site_2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."

ORIGIN
Query Match 14.3%; Score 832.8; DB 14; Length 872;
Best Local Similarity 99.2%; Pred. No. 8.1e-200;
Matches 831; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      3846 TTTTCGGGAAATGTGCGGGAACCCCTATTGTTGTTATTTCTTAAATACATTCAATAT 3905
Db      35 TTTTCGGGAAATGTGCGGGAACCCCTATTGTTGTTATTTCTTAAATACATTCAATAT 94

QY      3906 GTATCCGCTCATGAGACAATAACCTGATAAATGCTTCATAATATTGAAAGGAAGAG 3965
Db      95 GTATCCGCTCATGAGACAATAAACCCTGATAAATGCTTCATAATATTGAAAGGAAGAG 154

QY      3966 TATGAGTATTCACATTTCCGTCGTCCTTATTCCTTTTTCGGGCAATTTGCTTCC 4025
Db      155 TATGAGTATTCACATTTCCGTCGTCCTTATTCCTTTTTCGGGCAATTTGCTTCC 214

QY      4026 TGTTTTCTCACCAGAAAACGCTGTGGAAGTAAAGATGCTGAAGATCAGTTGGGTGC 4085
Db      215 TGTTTTCTCACCAGAGACGCTGTGGAAGTAAAGATGCTGAAGATCAGTTGGGTGC 274

QY      4086 ACGAGTGGTTACATCGAACTGGATCTCAACAGCGGTAAAGTCTTTCAGAGTTTTCGCC 4145
Db      275 ACGAGTGGTTACATCGAACTGGATCTCAACAGCGGTAAAGTCTTTCAGAGTTTTCGCC 334

1146 CGAAGAACGTTTTCATATGATGACACTTTTAAAGTTCTGCTATGTGCGGGTATTATC 4205
335 CGAAGAACGTTTTCATATGATGACACTTTTAAAGTTCTGCTATGTGCGGGTATTATC 394
4206 CCGTATTGACGCGCGGGAAGCAACTCGGTGCGGCATACACTATTCTCAGAATGACTT 4265
395 CCGTATTGACGCGCGGGAAGCAACTCGGTGCGGCATACACTATTCTCAGAATGACTT 454
4266 GTTTGAGTACTCACCAGTCAAGAAAAGCACTTTACGGATGGCATGACAGTAAGAAT 4325
455 GTTTGAGTACTCACCAGTCAAGAAAAGCACTTTACGGATGGCATGACAGTAAGAAT 514
4326 ATGAGTGTCTGCTATACCATGATGATAAACAACCTGCGGCCCACTTACTTCTGACAACGAT 4385
515 ATGAGTGTCTGCTATACCATGATGATAAACAACCTGCGGCCCACTTACTTCTGACAACGAT 574
4386 CCGAGGACCGAAGGAGCTAAACCGCTTTTTCGACAACTATGAGGATCATGTAACCTGCT 4445
575 CCGAGGACCGAAGGAGCTAAACCGCTTTTTCGACAACTATGAGGATCATGTAACCTGCT 634
4446 TGATCTGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGAT 4505
635 TGATCTGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGAT 694
4506 GCCTGTAGCAATGGCAACAACGTTGCGCAACTATTAACTGCGCACTACTTACTCTAGC 4565
695 GCCTGTAGCAATGGCAACAACGTTGCGCAACTATTAACTGCGCACTACTTACTCTAGC 754
4566 TTCCCGGCAACAATTAATAGACTGGATGGAGCGGATGAAAGTTGCAAGCACTTCTGCG 4625
755 TTCCCGGCAACAATTAATAGACTGGATGGAGCGGATGAAAGTTGCAAGCACTTCTGCG 814
4626 CTCGGCCCTTCCGGCTGGCTGTTTATGCTGATTAATCTGAGCCGCTGAGCGTGGG 4683
815 CTCGGCCCTTCCGGCTGGCTGTTTATGCTGATTAATCTGAGCCGCTGAGCGTGGG 872

RESULT 10
CF269652/c 1073 bp mRNA linear EST 13-AUG-2003
LOCUS      Fcylcol4844 Fragilariopsis cylindrus SMART cDNA library (Clontech)
DEFINITION  Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION  CF269652
VERSION    CF269652.1 GI:33631539
SOURCE     EST.
ORGANISM   Fragilariopsis cylindrus
Fragilariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
REFERENCE  1 (bases 1 to 1073)
AUTHORS   Mock, T. and Valentin, K.
TITLE     EST analysis of freezing tolerance in the Antarctic diatom
Fragilariopsis cylindrus: Detection of numerous cold adaptation
related genes and gene transfer events
JOURNAL   Unpublished (2003)
COMMENT   Contact: Mock T
Biological Oceanography
Alfred-Wegener-Institute for Polar and Marine Research
Am Handelshafen 12, D-27570 Bremerhaven, Germany
Tel: +49 471 4831 1893
Fax: +49 471 4831 1425
Email: tmock@awi-bremerhaven.de
PCR Primers
SEQUENCE WITH UNKNOWN FUNCTION
BACKWARD: 5' lambdaTriplex2
FORWARD: 3' lambdaTriplex2
Seq primer: ctcgggaagcgccattgtgtgtt.
Location/Qualifiers
1..1073
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/strain="Antarctic"
FEATURES
Source

```


/db_xref="taxon:186039"
/clone="Antarctic"
/clone_lib="Fragilariopsis cylindrus SMART cDNA library
(Clontech)"
/note="vector: pTriplex2; total polyA was used for
first-strand synthesis with SMART IV oligos and CDS
III/3 PCR primer. Double strand cDNA synthesis was done by
LD PCR using the following program: 95°C for 5 min
denaturation and subsequent 20 cycles at 95°C (2min) and
68°C (6min). After SfiI digestion the cDNA was
fractionated with CHROMA Spin-400 columns. These cDNAs
were ligated overnight into pTriplex2 vectors."

ORIGIN

Query Match 14.2%; Score 825; DB 14; Length 1073;
Best Local Similarity 96.5%; Pred. No. 8.1e-198;
Matches 884; Conservative 0; Mismatches 25; Indels 7; Gaps 4;

QY 4914 TGATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCACCTGAGCGTCAGACCC 4973
DB 964 TTATTGTCTCATGCCAAATCCCTTAACTGAGTTTTCGTTCACCTGAGCGTCAGACCC 905
QY 4974 CGTAGAAAAGATCAAGAGATCTCTTGAGATCTCTTTTCTGCGGTAACTCTGCTCTT 5033
DB 904 CGTAGAAAAGATCAAGAGATCTCTTGAGATCTCTTTTCTGCGGTAACTCTGCTCTT 845
QY 5034 GCAACAAAAAACCACCGCTTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 5093
DB 844 GCAACAAAAAACCACCGCTTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 785
QY 5094 TCTTTTCCGAGTAACT--GGCTTCAGCAGAGCGC-AGATACCAATAC-TGTCTT 5148
DB 784 TCTTTTCCGAGTAACTGCTTTCNAGCAGAGCGCAGATACCAATAC-TGTCTT 725
QY 5149 CTAGTGTAGCG--TAGTTAGGCACACACTTCAAGAACTCTGAGACCGCCTACAPAC 5206
DB 724 CTAGTGTAGCGTAGTTANGGCGCCACTTCAAGAACTCTGAGACCGCCTACAPAC 665
QY 5207 TCCTCTGCTAATCTTGTACAGTGTCTGCTGCGAGTGGGATAGTCTGTCTTACCG 5266
DB 664 TCCTCTGCTAATCTTGTACAGTGTCTGCTGCGAGTGGGATAGTCTGTCTTACCG 605
QY 5267 GGTGGACTCAAGACGATGTTACCGGATAAGCGCAGCGCTCGGCTGAAACGGGGGTT 5326
DB 604 GGTGGACTCAAGACGATGTTACCGGATAAGCGCAGCGCTCGGCTGAAACGGGGGTT 545
QY 5327 CGTGACACAGCCCGCTTGAGCGGACGACCTACCGAACTGAGATACCTACAGCGT 5386
DB 544 CGTGACACAGCCCGCTTGAGCGGACGACCTACCGAACTGAGATACCTACAGCGT 485
QY 5387 AGCTATGAGAAAGCGCCAGCTTCCGAGGAGGAGAAAGCGGATCCGCTGATCTTT 5446
DB 484 AGCTATGAGAAAGCGCCAGCTTCCGAGGAGGAGAAAGCGGATCCGCTGATCTTT 425
QY 5447 GCAGGTCGGAACAGAGAGCGCACAGGAGCTTCCAGGGGAAACGGCTGATCTTT 5506
DB 424 GCAGGTCGGAACAGAGAGCGCACAGGAGCTTCCAGGGGAAACGGCTGATCTTT 365
QY 5507 ATAGTCTCGGTTTCGCCACCTTGATGAGCGTGAATTTTGTGATGCTGCTAG 5566
DB 364 ATAGTCTCGGTTTCGCCACCTTGATGAGCGTGAATTTTGTGATGCTGCTAG 305
QY 5567 GGGGGCGGAGCTATGAAAAAGCGCAGAAACGGGCTTTTACGGTTCTCGGCTTTT 5626
DB 304 GGGGGCGGAGCTATGAAAAAGCGCAGAAACGGGCTTTTACGGTTCTCGGCTTTT 245
QY 5627 GTGGCTTTTCTCATGTTCTTTCCTCGGTTATCCCTGATCTGTGGATAACCGTA 5686
DB 244 GTGGCTTTTCTCATGTTCTTTCCTCGGTTATCCCTGATCTGTGGATAACCGTA 185
QY 5687 TTACCGCTTTGAGTGAAGTGAATACCGCTCGCGCAGCGCAACGACCGAGCGAGCT 5746
DB 184 TTACCGCTTTGAGTGAAGTGAATACCGCTCGCGCAGCGCAACGACCGAGCGAGCT 125

QY 5747 CAGTAGCGAGGAGGAGCGGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTGGC 5806
DB 124 CAGTAGCGAGGAGGAGCGGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTGGC 65
QY 5807 CGATTCTAATATGCGAG 5822
DB 64 CGATTCTAATATGCGAG 49

RESULT 11
LOCUS BM438950
DEFINITION Ipluvr00491 Liver cDNA library Ictalurus punctatus cdna 5', mRNA
ACCESSION BM438950
VERSION BM438950.1 GI:18460672
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 854)
Feng, J.; Kucuktas, H.; Kocabas, A., Li, P. and Liu, Z.
Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
Unpublished (2002)
Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
1..854
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cDNA library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: Sall"

ORIGIN

Query Match 14.2%; Score 824.6; DB 12; Length 854;
Best Local Similarity 99.3%; Pred. No. 9.7e-198;
Matches 849; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 4012 GCATTTTGCTTCTCTGTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGTGTGAA 4071
DB 1 GCATTTTGCTTCTCTGTTTGTCTACCCAGATACGCTGGTGAAGTAAAGTGTGAA 60
QY 4072 GATCATGTTGGGTGACAGTGGG-TTACATCGAACTGGATCTCAACAGCGTAAGATCTT 4130
DB 61 GATCATGTTGGGTGACAGTGGGCTTACATCGAACTGGATCTCAACAGCGTAAGATCTT 120
QY 4131 TGAGAGTTTTCGCCCGGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATG 4190
DB 121 TGAGAGTTTTCGCCCGGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATG 180
QY 4191 TGGCGCGGTATTATCCCGTATTGACCGGGCAAGCAACTCGGTCCGCGCATACACTA 4250
DB 181 TGGCGCGGTATTATCCCGTATTGACCGGGCAAGCAACTCGGTCCGCGCATACACTA 240
QY 4251 TTCTCAGAAATGACTTGGTTGAGTACTCAACAGTACAGAAAGCAATCTTACGGATGGCAT 4310
DB 241 TTCTCAGAAATGACTTGGTTGAGTACTCAACAGTACAGAAAGCAATCTTACGGATGGCAT 300
QY 4311 GACAGTAAGAGAAATTATGCAAGTGTGTCCTAATACCATGAGTGATACACTGCGCGCAACTT 4370

```
Db 301 GACAGTAAGAGAAATATGACGTGTCCTCAATCAACATGATGATTAACACTGCGCCAACTT 360
Qy 4371 ACTTCTGACAAACGATCGGAGACCGAAGAGCTAACCGCTTTTGTGCAACATGGGGGA 4430
Db 361 ACTTCTGACAAACGATCGGAGACCGAA-GAGCTAACCGCTTTTGTGCAACATGGGGGA 419
Qy 4431 TCATGTAACCTGCCCTTGATCGTTGGGAACCGAGTGAATGAAGCCATACCAACGACGA 4490
Db 420 TCATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGA 479
Qy 4491 GCGTGACACACGATGCTGTAGCAATGCGCAACACGCTTGCGCAAACTATTAACTGGCGA 4550
Db 480 GCGTGACACACGATGCTGTAGCAATGCGCAACACGCTTGCGCAAACTATTAACTGGCGA 539
Qy 4551 ACTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGGGGATTAAGTTGC 4610
Db 540 ACTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGGGGATTAAGTTGC 599
Qy 4611 AGGACACCTCTGCGCTCGGCCCTTCCGCTCGCTGCTGTTTATTGCTGATAAATCTGGAGC 4670
Db 600 AGGACACCTCTGCGCTCGGCCCTTCCGCTCGCTGCTGTTTATTGCTGATAAATCTGGAGC 659
Qy 4671 CGGTGAGCGTGGCTCTCGCGGTATCATTGCGACACTGGGGCCAGATGCTTAAGCCCTCCCG 4730
Db 660 CGGTGAGCGTGGCTCTCGCGGTATCATTGCGACACTGGGGCCAGATGCTTAAGCCCTCCCG 719
Qy 4731 TATCGTAGTATPCTACAGACGGGAGTCAGGCAACTATGATGAACGAATAGACAGAT 4790
Db 720 TATCGTAGTATPCTACAGACGGGAGTCAGGCAACTATGATGAACGAATAGACAGAT 779
Qy 4791 CGGTGAGTGTGCTCTACTGATTAAGCAATGTTAACTGTCAGACCAAGTTTACTCATA 4850
Db 780 CGGTGAGTGTGCTCTACTGATTAAGCAATGTTAACTGTCAGACCAAGTTTACTCATA 839
Qy 4851 TATACTTTAGATTGA 4865
Db 840 TATGCTTGAGATTGA 854
```

```
RESULT 12
CD458333
LOCUS
DEFINITION
Fg08_09e07_R Fg08_AAFRC_EOORC_Fusarium_graminearum_complex_substrate
Gibberella zeae cDNA clone Fg08_09e07, mRNA sequence.
ACCESSION
CD458333
VERSION
CD458333.1 GI:31373073
KEYWORDS
EST.
SOURCE
Gibberella zeae
ORGANISM
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 870)
AUTHORS
Watson,R.J., Heys,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
TITLE
A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
JOURNAL
Unpublished (2003)
COMMENT
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
FEATURES
Location/Qualifiers
source
1..870
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
```

```
/clone="Fg08_09e07"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAFRC_EOORC_Fusarium_graminearum_complex_s
ubstrate"
/note="vector: pBluescript II+; Site_1: EcoRI; Site_2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
ORIGIN
Query Match 14.1%; Score 819.6; DB 14; Length 870;
Best Local Similarity 99.2%; Pred. No. 1.8e-196;
Matches 841; Conservative 3; Mismatches 2; Indels 2; Gaps 2;
Qy 3833 ATACAGGTGGCACATTTTCGGGGAATGTGCGCGGAACCCCTATTTGTTTATTTCTAAA 3892
Db 24 ATTTAGGTGGCASTTTTCGGGGAATGTGCGCGGAACCCCTATTTGTTTATTTCTAAA 83
Qy 3893 TACATTCAAAATATGATCCGCTCATGAGACAATAAACCTGTATAATGCTTCAATAATTT 3952
Db 84 TACATTCAAAATATGATCCGCTCATGAGACAATAAACCTGTATAATGCTTCAATAATTT 143
Qy 3953 GAAAAAGGAGATGATGATTTCAACATTTCCGTGTCGCCCTTATTCCTTTTTCGCG 4012
Db 144 GAAAAAGGAGATGATGATTTCAACATTTCCGTGTCGCCCTTATTCCTTTTTCGCG 203
Qy 4013 CATTTTGCCTTCTCTTTTGTCTACCCAGAACCGCTGGTGAAGTAAAGATGCTGAAG 4072
Db 204 CATTTTGCCTTCTCTTTTGTCTACCCAGAACCGCTGGTGAAGTAAAGATGCTGAAG 263
Qy 4073 ATCAGTTGGGTGCACGAGTGGTTACATCGAATCTGGAATCTAACAGCGGTAGATCCTTG 4132
Db 264 ATCAGTTGGGTGCACGAGTGGTTACATCGAATCTGGAATCTAACAGCGGTAGATCCTTG 323
Qy 4133 AGAGTTTTCGCCCGGAGAACGTTTTCGAATGATGACACTTTTAAAGTTCTCTATGTG 4192
Db 324 AGAGTTTTCGCCCGGAGAACGTTTTCGAATGATGACACTTTTAAAGTTCTCTATGTG 383
Qy 4193 GCGCGTATTTATCCCGTATTTGACCGCGGCAAGAGCAACTCGCTGCCCGCATACACTATT 4252
Db 384 GCGCGTATTTATCCCGTATTTGACCGCGGCAAGAGCAACTCGCTGCCCGCATACACTATT 443
Qy 4253 CTCAGAAATGACTTGGTTGATCTACCGAGTCTACAGAAAGCATCTTACGGATGGATGA 4312
Db 444 CTCAGAAATGACTTGGTTGATCTACCGAGTCTACAGAAAGCATCTTACGGATGGATGA 503
Qy 4313 CAGTAAGAGAAATTTATGCACTGCTGCCATTAACCATGATGATAACACTGCGGCCAATTCAC 4372
Db 504 CAGTAAGAGAAATTTATGCACTGCTGCCATTAACCATGATGATAACACTGCGGCCAATTCAC 563
Qy 4373 -TTCTGCAACAGATCGGAGACCGAAGGAGCTAACCGCTTTTTCGCAACATGGGGGAT 4431
Db 564 TTTCTGCAACAGATCGGAGACCGAA-GAGCTAACCGCTTTTTCGCAACATGGGGGAT 622
Qy 4432 CATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 4491
Db 623 CATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 682
Qy 4492 CGTGACACACGATGCTGTAGCAATGCGCAACACGCTTGCGCAAACTATTAACTGGCGAA 4551
Db 683 CGTGACACACGATGCTGTAGCAATGCGCAACACGCTTGCGCAAACTATTAACTGGCGAA 742
Qy 4552 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGGGGATTAAGTTGCA 4611
Db 743 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGGGGATTAAGTTGCA 802
Qy 4612 GGACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGTTTATTCGTGATAATCTGAGGCC 4671
Db 803 GGACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGTTTATTCGTGATAATCTGAGGCC 862
Qy 4672 GGTGAGCG 4679
```

```

Db      863  GKGAGCG 870

RESULT 13
BZ572284/c
LOCUS   BZ572284      1249 bp    DNA        linear    GSS 17-DEC-2002
DEFINITION msh2_2572.x3 msh Pseudomonas aeruginosa genomic clone msh2_2572,
            genomic survey sequence.
ACCESSION BZ572284
VERSION   BZ572284.1 GI:27207345
KEYWORDS  GSS
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1249)
AUTHORS   Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
            Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE     Whole-Genome-Sequence Variation among multiple isolates of
            Pseudomonas aeruginosa library
JOURNAL   J. Bacteriol. (2002) In press
COMMENT   Contact: Chris K. Raymond
            Genome Center
            University of Washington
            Box 352145, Seattle, WA 98105-2145, USA
            Tel: 2062216954
            Fax: 2066857244
            Email: craymond@u.washington.edu
            Class: shotgun.

FEATURES             source
     source
     1..1249
         /organism="Pseudomonas aeruginosa"
         /mol_type="genomic DNA"
         /strain="MSH"
         /db_xref="taxon:287"
         /clone="msh2_2572"
         /clone_lib="msh"
         /notes="Environmental isolate. Whole genomic shotgun
            library."

ORIGIN
Query Match      14.0%; Score 815.6; DB 28; Length 1249;
Best Local Similarity 93.0%; Pred. No. 2e-195;
Matches 952; Conservative 0; Mismatches 61; Indels 11; Gaps 9;

QY      4799  TAGTGCCCTCAGTAAAGCAATGGTGAAGTGTGACAGCAAGTTTACTCATATATCTTT 4858
Db      1116  TATGGGCCCCCAGATATAACACTGGGGACCCGACAGCAAGTTTCCCCA-AAATAACTT 1058
QY      4859  AGATTGATTAAACACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGATA 4918
Db      1057  AAATTGATTAAACACTTCC-TTTTATTTAAAGGATTAAGGT-AAAGATCCTTTTAAAA 1000
QY      4919  ATCTATGACCAAAATCCCTTAACGTGAGTTTTCGTTCACCTGAGCGTCAGACCCCGTAG 4978
Db      999  ATCTCATG--CCAAAATCCCTTACGTGAGTTTTCGTTCACCTAAGGGCCAGACCCGTA 942
QY      4979  AAAAGATCAAGAGATCTTCTTGAGATCCCTTTTTCGCGGTAACTCTGCTGCTGCAAA 5038
Db      941  GAAAGACCAAGATCTTCTGAGAACCTTTTTCGTGCGGTAAT-TGCTGCTGTC-AA 884
QY      5039  CAAAAAACCCCGCTTACAGCGGGTGTGTTGTTGCGGATCAAGAGCTACCACTCTTT 5098
Db      883  CAAAAAACCCCGCTTACAGCGGTGTTG--TTTGGCGATCAAGAGCTA-CAACTCTTT 827
QY      5099  TTCCGAGTAACTGGCTTACAGAGCGCAGATACCAAAATCTGTCCTTCTAGTGTAGC 5158
Db      826  TTCGAGAGGTANCT-GCTTACAGAGCGCAGATACCAAAATCTGTTCTTCTAGTGTAGC 768
QY      5159  CTTAGTTAGGCCACCACTTCAGAACTCTGTAGACCGGCTTACATCTGCTCTGTAA 5218
Db      767  GGTAGTTAGGCCACCACTTCAGAACTCTGTAGACCGGCTTACATCTGCTCTGTAA 708

5219  TCCTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAA 5278
707   TCCTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAA 648
5279  GACGATAGTTACCGGATAAGGGCGAGCGGTGGGCTGAACGGGGGTTGCTGCACACAGC 5338
647   GACGATAGTTACCGGATAAGGGCGAGCGGTGGGCTGAACGGGGGTTGCTGCACACAGC 588
5339  CCAGCTTGGAGCGCAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAA 5398
587   CCAGCTTGGAGCGCAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAA 528
5399  GCGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGAGGGTCGAA 5458
527   GCGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGAGGGTCGAA 468
5459  CAGGAGCGCGCAGGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTCTGTCG 5518
467   CAGGAGCGCGCAGGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTCTGTCG 408
5519  GGTTCGCCACCTCTGACTTGAAGCGTGAATTTTGTGATGCTGCTCAGGGGGGCGAGCC 5578
407   GGTTCGCCACCTCTGACTTGAAGCGTGAATTTTGTGATGCTGCTCAGGGGGGCGAGCC 348
5579  TATGGAAGAAACGCGCAGCAACCGGCGCTTTTACGGTTCTCTGGCCTTTTGTGGCCTTTTG 5638
347   TATGGAAGAAACGCGCAGCAACCGGCGCTTTTACGGTTCTCTGGCCTTTTGTGGCCTTTTG 288
5639  CTCACATGTTCTTCTGCGCTTATCCCTGATTTCTGATCTGTGATTAACCGTATTAACGCCCTTTG 5698
287   CTCACATGTTCTTCTGCGCTTATCCCTGATTTCTGATCTGTGATTAACCGTATTAACGCCCTTTG 228
5699  AGTGAGCTGATACCGCTCGCGCAGCAACCGGCGCTTTTACGGTTCTCTGGCCTTTTGTGGCCTTTTG 5758
227   AGTGAGCTGATACCGCTCGCGCAGCAACCGGCGCTTTTACGGTTCTCTGGCCTTTTGTGGCCTTTTG 168
5759  AAGCGAAGAGCGCCCAATACGCAACCGCTCTCCCGCGCGCTTGGCCGATTCATTAAAT 5818
167   AAGCGAAGAGCGCCCAATACGCAACCGCTCTCCCGCGCGCTTGGCCGATTCATTAAAT 108
5819  GCAG 5822
107   GCAG 104

RESULT 14
BZ577702
LOCUS   BZ577702      1126 bp    DNA        linear    GSS 17-DEC-2002
DEFINITION msh2_5533.y2 msh Pseudomonas aeruginosa genomic clone msh2_5533,
            genomic survey sequence.
ACCESSION BZ577702
VERSION   BZ577702.1 GI:27212763
KEYWORDS  GSS
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 1126)
AUTHORS   Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
            Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE     Whole-Genome-Sequence Variation among multiple isolates of
            Pseudomonas aeruginosa library
JOURNAL   J. Bacteriol. (2002) In press
COMMENT   Contact: Chris K. Raymond
            Genome Center
            University of Washington
            Box 352145, Seattle, WA 98105-2145, USA
            Tel: 2062216954
            Fax: 2066857244
            Email: craymond@u.washington.edu
            Class: shotgun.
            Location/Qualifiers
FEATURES

```

source 1. 1126 /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="MSH" /db_xref="taxon:287" /clone_lib="mh2 5533" /clone_lib="mh" /note="Environmental isolate. Whole genomic shotgun library."

ORIGIN

Query Match 14.0%; Score 814.4; DB 28; Length 1126; Best Local Similarity 90.4%; Pred. No. 4e-195; Matches 938; Conservative 0; Mismatches 91; Indels 9; Gaps 6;

QY 3881 TATTTTCTAAATACATTCAAATATGATCGCTCATGAGACAATAACCTGATAAATGC 3940

Db 93 TATTTTCTAAATACATTCAAATATGATCGCTCATGAGACAATAACCTGATAAATGC 152

QY 3941 TTCAATATATTTGAAAAGGAGATGATGATTTCAACATTTCCGTGTCGCCCTTATTC 4000

Db 153 TTCAATATATTTGAAAAGGAGATGATGATTTCAACATTTCCGTGTCGCCCTTATTC 212

QY 4001 CTTTTTTTGGCCATTTTGCCTTCTCTTTTCTCACCAGAAACGCTGGTGAAGTAA 4060

Db 213 CTTTTTTTGGCCATTTTGCCTTCTCTTTTCTCACCAGAAACGCTGGTGAAGTAA 272

QY 4061 AAGATGCTGAAGATCATGTTGGTGCACGAGTGGTTACATCACTGGATCTCAACAGCG 4120

Db 273 AAGATGCTGAAGATCATGTTGGTGCACGAGTGGTTACATCACTGGATCTCAACAGCG 332

QY 4121 GTAAGATCTTTGAGATTTTCCGCCGGAAGAACGTTTCCAAATGATGAGCACTTTTAAAG 4180

Db 333 GTAAGATCTTTGAGATTTTCCGCCGGAAGAACGTTTCCAAATGATGAGCACTTTTAAAG 392

QY 4181 TTCTGCTATGTGGCGGGTATTATCCGCTATTGACCGCGGGCAAGAGCAACTCGGTGCGC 4240

Db 393 TTCTGCTATGTGGCGGGTATTATCCGCTATTGACCGCGGGCAAGAGCAACTCGGTGCGC 452

QY 4241 GCATACATTTCTCAGATGATCTGGTTGAGTACTACCACTGACAGAAAGCATCTTA 4300

Db 453 GCATACATTTCTCAGATGATCTGGTTGAGTACTACCACTGACAGAAAGCATCTTA 512

QY 4301 CGGATGGCATGACAGTAAGAGAATATGCGAGTCTGCTGATTAACCATGAGTGAATAACTG 4360

Db 513 CGGATGGCATGACAGTAAGAGAATATGCGAGTCTGCTGATTAACCATGAGTGAATAACTG 572

QY 4361 CGGCCAACTTACTTCTGACAAACGATCGGAGGACGAGGAGCTAACCGCTTTTTCGACA 4420

Db 573 CGGTCAACTTACTTCTGACAAACGATCGGAGGACGAGGAGCTAACCGCTTTTTCGACA 632

QY 4421 ACATGGGGATCATGTAATCTCGCTTGTATCGTTGGGAACCGAGCTGAATGAGCCATAC 4480

Db 633 ACATGGGGATCATGTAATCTCGCTTGTATCGTTGGGAACCGAGCTGAATGAGCCATAC 692

QY 4481 CAAACGACGCGGTGACACACGATGCTGTAGCAATGGCAACACGCTGCGCAAACTAT 4540

Db 693 CAAACGACGCGGTGACACACGATGCTGTAGCAATGGCAACACGCTGCGCACTAT 752

QY 4541 TAACTGGCGAATCTTACTTCTAGCTTTCCCGGCAACAATTAATAGATGAGTGGAGCGG 4600

Db 753 TAACTGGCGAATCTTACTTCTAGCTTTCCCGGCAACAATTAATAGATGAGTGGAGCGG 812

QY 4601 AT-AAAAGTTGAGGACACATCTTCTGCGCTCGGCCCTTCCGCTGGCTGGTTTATGCTGAT 4659

Db 813 ATAAAAGTTGAGGACACATCTTCTGCGCTCGGCCCTTCCGCTGGCTGGTTTATGCTGAT 872

QY 4660 AAATCTGAGCGGTGACGCTGGGTCTCGCGGTATCATTTGACGACTCGGGCCAGATGGT 4719

Db 873 TAAATTTGAGCGCGGGAACGGGGCTTCGCGGTACATTTGACTTCTGCTGCTGCTGCTGCT 932

QY 4720 AAGCCCTCCCGTATCGTATGTTATCTACAGA-CGGGGAGTCAAGCAACTA-TGGATGAAC 4777

933 AAACCCCTCCGATCGGAATTTTCTACCGACCGGGAGTCAGGAACTATTGTTTAAAC 992

QY 4778 GAAATAGACAGATCGCTGAGAT-AGGTGCTCCTACGATTAGCACTTGGTAACTGCAGAC 4836

Db 993 GAAATAGACAGATAGCCTTGATAAGGGCCCTTCATGATATATAACTTTTGAACACTGTCGAA 1052

QY 4837 CAAGTTTACTCATATATATCTTACATTTAGATTTAAACCTTCATTTTAAATTTAAAGGATC 4896

Db 1053 CAAGTTTACTC--AAATACCTTAAATGATTTAAACCTTC--TTTATATTAAGGGTC 1107

QY 4897 TAGGTGAAGATCCTTTT 4914

Db 1108 TAGGAGAGAAACCTTTT 1125

RESULT 15

CD649375 819 bp mRNA linear EST 18-JUN-2003

LOCUS Cvsnd00080 Crassostrea virginica Gonad Crassostrea virginica cDNA

DEFINITION 5', mRNA sequence.

ACCESSION CD649375

VERSION CD649375.1 GI:31906346

KEYWORDS EST.

SOURCE Crassostrea virginica (eastern oyster)

ORGANISM Crassostrea virginica

Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida; Ostreidae; Ostreidae; Crassostrea.

REFERENCE 1 (bases 1 to 819)

AUTHORS Peatman,E., Kucuktas,H., Li,P., He,C., Feng,J., Wei,X. and Liu,Z.

TITLE Differentially expressed oyster (Crassostrea virginica) genes after exposure to mercury

JOURNAL unpublished (2003)

COMMENT Contact: Liu Z

The Fish Molecular Genetics and Biotechnology Laboratory, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences

Auburn University

201 Swingle Hall, Auburn University, Auburn, AL 36849, USA

Tel: 334 844 4054

Fax: 334 844 9208

Email: zliu@acesag.auburn.edu

Seq primer: M13 Reverse.

FEATURES

source 1. 819

/organism="Crassostrea virginica"

/mol_type="mRNA"

/db_xref="taxon:6565"

/clone_lib="Crassostrea virginica Gonad"

/note="Organ: Gonad; Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 13.9%; Score 808; DB 14; Length 819; Best Local Similarity 99.9%; Pred. No. 1.6e-193; Matches 819; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4012 GCATTTTGCCTTCTCTTTTGTCTCACCAGAACGCTGGTGAAGTAAAGATGCTGAA 4071

Db 1 GCATTTTGCCTTCTCTTTTGTCTCACCAGAACGCTGGTGAAGTAAAGATGCTGAA 60

QY 4072 GATCAGTTGGTGCACAGTGGGTACATCGAACTGGATCTCAACAGCGTAAAGTCTT 4131

Db 61 GATCAGTTGGTGCACAGTGGGTACATCGAACTGGATCTCAACAGCGTAAAGTCTT 120

QY 4132 GAGAGTTTTCGCCCGGAGAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 4191

Db 121 GAGAGTTTTCGCCCGGAGAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 180

QY 4192 GGCGCGGTATTTATCCCGTATTTGACCGGGCAAGCAACTCGGTTCGCCGATACACTAT 4251

Db 181 GGCGCGGTATTTATCCCGTATTTGACCGGGCAAGCAACTCGGTTCGCCGATACACTAT 240

QY 4252 TCTCAGATGACTGTTGTTGACTACTCACCAGTCAAGAAAAGCATCTTACCGATGGCATG 4311

```
Db      241  TCTCAGATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTTACGGATGGCATG 300
Qy      4312  ACAGTAAAGAGAAATTATGAGTCTGCCATACCATGATGATGATACACTGGCGGCCAACTTA 4371
Db      301  ACAGTAAAGAGAAATTATGAGTCTGCCATACCATGATGATGATGATGATGATGATGATGAT 360
Qy      4372  CTTCTGACAAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTCGACAAACATGGGGAT 4431
Db      361  CTTCTGACAAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTCGACAAACATGGGGAT 419
Qy      4432  CATGTAACCTGCCCTTGATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAAAACGACGAG 4491
Db      420  CATGTAACCTGCCCTTGATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAAAACGACGAG 479
Qy      4492  CGTGACACCAAGATGCTGTAGCAATGCAACACGCTTGGCAAACTATTAACCTGGCGAA 4551
Db      480  CGTGACACCAAGATGCTGTAGCAATGCAACACGCTTGGCAAACTATTAACCTGGCGAA 539
Qy      4552  CTAATTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGCGGATAAAGTTGCA 4611
Db      540  CTAATTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGCGGATAAAGTTGCA 599
Qy      4612  GGACCACTTCTGGCTCGGCCCTTCCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCC 4671
Db      600  GGACCACTTCTGGCTCGGCCCTTCCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCC 659
Qy      4672  GGTGAGCGTGGGTCTCGCGTATCATTCAGCACTGGGCGGAGATGGTAAAGCCCTCCCGT 4731
Db      660  GGTGAGCGTGGGTCTCGCGTATCATTCAGCACTGGGCGGAGATGGTAAAGCCCTCCCGT 719
Qy      4732  ATCGTAGTTATCTACACGACGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATC 4791
Db      720  ATCGTAGTTATCTACACGACGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATC 779
Qy      4792  GCTGAGATAGGTGCTCCTACGTAAAGCATTTGGTAACTGT 4831
Db      780  GCTGAGATAGGTGCTCCTACGTAAAGCATTTGGTAACTGT 819
```

Search completed: June 21, 2004, 21:28:44
Job time : 8922 secs

This Page Blank (uspto)

This Page Blank (uspto)